



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 176764

TO: Walter Schlapkohl
Location: rem/2b79/2c70
Art Unit: 1636
Tuesday, January 17, 2006
Case Serial Number: 09/671687

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes



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[Text Entry](#) | [EmblEntry](#)

Go to: [General](#) [Description](#) [References](#) [Cross-references](#) [Sequence](#)

General Information

Primary Accession # AJ250014
Accession # AJ250014
Entry Name EMBL:HSA250014
Molecule Type mRNA
Sequence Length 5371
Entry Division HUM
Sequence Version AJ250014.1
Creation Date 03-JUN-2000
Modification Date 16-JUN-2000

Description

Description Homo sapiens mRNA for Familial Cyndromatosis cyld gene
Keywords cyld gene; Familial Cyndromatosis.;
Organism Homo sapiens (human)
Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheri
Classification Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

References

1. Stratton,M.R.; Submitted (29-NOV-1999) to the EMBL/GenBank/DDBJ databases. Stratton M.R., Cancer Genetics, Institute of Cancer Research, 15 Cotswold Rd, Sutton,, Surrey. S15 2NT, UNITED KINGDOM.
Position 1-5371
2. Bignell,G.R.; Brown,C.; Biggs,P.J.; Lakhani,S.R.; Jones,C.; Hansen,J.; Blair,E.; Hofmann Siebert,R.; Turner,G.; Evans,D.G.; Schrander-Stumpel,C.; Beemer,F.A.; Van Den Ouwe Halley,D.; Delpech,B.; Cleveland,M.G.; Leigh,I.; Leisti,J.; Rasmussen,S.; Wallace,M.R.; Fenske,C.; Banerjee,P.; Oiso,N.; Chaggar,R.; Merrett,S.; Leonard,N.; Huber,M.; Hohl,D Chapman,P.; Burn,J.; Swift,S.; Smith,A.; Ashworth,A.; Stratton,M.R.;
Identification of the familial cyndromatosis tumor suppressor gene.
Nat. Genet. 25(2):160-165 (2000)
DOI [10.1038/76006](#)
Pubmed [10835629](#)

Database Cross-references

GDB [701216](#).

Features

Key	Location	Qualifier	Value
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		db_xref	<u>taxon:9606</u>
		mol_type	mRNA
		organism	Homo sapiens
		map	16q12 - q13
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		db_xref	<u>PDB:1WHM</u>
		db_xref	<u>UniProtKB/Swiss-Prot:Q9NQC7</u>
		note	Familial Cylindromatosis Gene
		gene	cyld
		function	tumour suppressor/recessive oncogene
		experiment	experimental evidence, no additional details reco
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Sequence

Characteristics	Length: 5371 BP, A Count: 1600, C Count: 950, G Count: 1183, T Count: 1638, Other: Count: 0
Sequence	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 23:03:04 ; Search time 9744 Seconds
(without alignments)
5385.028 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

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Fgapop 6.0			7.0
Delop 6.0			7.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 33

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	4983	99.0	4668	23	Sequence 4309, Ap

8 4983 99.0 4668 23 US-09-396-970-7559 Sequence 7559, Ap
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10 4983 99.0 4668 23 US-09-397-424A-5019 Sequence 5019, Ap
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18 4971.5 98.8 5371 33 US-09-851-673-3 Sequence 3, Appli
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24 4971.5 98.8 5371 83 US-60-710-726-1537 Sequence 1537, Ap
25 4970 98.7 6314 78 US-60-324-185-23812 Sequence 23812, A
26 4953 98.4 6315 76 US-60-213-359-5981 Sequence 5981, Ap
27 4953 98.4 6316 77 US-60-278-232-7384 Sequence 7384, Ap
28 4942 98.2 4527 32 US-09-786-797B-25 Sequence 25, Appl
29 4942 98.2 4527 63 US-10-921-707-25 Sequence 25, Appl
30 4942 98.2 4527 75 US-60-131-321-21 Sequence 21, Appl
31 4916 97.7 6315 75 US-60-172-360-22693 Sequence 22693, A
32 4601 91.4 2845 28 US-09-629-469A-18842 Sequence 18842, A
33 4601 91.4 2845 63 US-10-917-503-18842 Sequence 18842, A

ALIGNMENTS

RESULT 1
US-09-671-687a-2
Sequence 2, Application US/09671687A
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: KOVALENKO, Andrei
APPLICANT: CANTARELLA, Giuseppe
TITLE OF INVENTION: INHIBITOR OF NF-kB ACTIVATOR
FILE REFERENCE: WALLACH-25
CURRENT APPLICATION NUMBER: US/09/671,687A
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: IL 126024
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: IL 134604
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 3715
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ORGANISM: Homo sapiens
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US-09-671-687a-2

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Score: 4992.00 Matches: 949
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Best Local Similarity: 99.58% Mismatches: 0

Query Match: 99.17% Indels: 4
DB: 29 Gaps: 4
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Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 1037 TACCAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTCTTTGTGTCATTGGAC 1096
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 1097 AAGCTAGAACTCATAGAAGATGATGACATGTCATTGGAAAGTATTACGACAGGTCTCTGGG 1156
Qy 219 AspThrMetGlnValGluLeuProPheGluLeuLeuSerArgValSerLeuLysGly 238
Db 1157 GACAAATGCGAGTTCGAACTTCTCTTTCGAAATAAACTCCAGAGTTTCTTTGAAGGT 1216
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 1217 GGAGAAACAATAGAACTCTGGAAACAGTTATATCTGTGATGTTTTCAGGAGAAAAGAAC 1276
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1277 TTAGGATATTTTGTGTTGTTGTCGATGATGATGATGATGATGATGATGATGATGATGAT 1336
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1337 GATGGAGTGCANCTTTTGTAGTTTTTTCGCGTGTGTTGAAAGTACAAATTTCTATTGTCACA 1396
Qy 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
Db 1397 GATATCATCCAGAGAGTGTGACGAGAAAGAGGCGCTCCCAAACTTGCTTTTATGTCATCA 1456
Qy 318 ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1457 AGAGTGTGGGACAAAGGTTTCATCCAGTCATATAAACCAAGGCTACAGGATCTACC 1516

OTHER INFORMATION: n = A,T,C or G
US-09-522-303-1293

Alignment Scores:

Pred. No.:	0	Length:	4661
Score:	4983.00	Matches:	948
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	98.99%	Indels:	4
DB:	25	Gaps:	4

US-09-671-687A-3 (1-949) x US-09-522-303-1293 (1-4661)

Qy	1	MetSerSerGlyLeuTpsSerGlnGluLysValThrSerProTyrTrpGluGluArgile	20
Db	231	ATGAGTTTCAGCTTATGAGCAAGAAAGTCACTTCCCTACTGGGAAGCGGATT	290
Qy	21	PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrLysLeuLeuLys	40
Db	291	TTTTACTTGTCTTCAAGATGCGGTTACAGACAAACACAAAGCTCCTTAAA	350
Qy	41	ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgile	60
Db	351	GTACCGAAGGAGATATAGGACAGTATATCAAGATCGTTCTGTGGGCGCATTC	410
Qy	61	ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla	80
Db	411	CCITCTGCAAGGCAAGAAATCAGATTGGATTAAATAATCTAGAGCAACCTCAT	470
Qy	81	ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeu	99
Db	471	GTTCTCTTTGTTGATGAAGGATGTTGTAGAGATAAATGAAGATTTCACAGATT	530
Qy	100	LeuAlaIleThrAsnCysGluGluAurPheSerLeuPheLysAsnArgLeuSer	119
Db	531	TTGGCAATTACCAATTGTGAGGAGAGGTCAGCCCTGTTTAAAAACAGAAAC	590
Qy	120	LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGlu	139
Db	591	AAAGGCTCCAAATAGACGCGGGCTGCTGTGTAAGTACAGCTGAGATCTGG	650
Qy	140	LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSer	159
Db	651	AAATTTCTGGAGTTGTACGCTTCAGAGGCCCTGTTAGCAGAGAGACAGTCT	710
Qy	160	IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGly	179
Db	711	ATATTTCTTGGAGTTGAATTGCTGGAAGAGGTCGTGTCAGGTTTCACTGAC	770
Qy	180	TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeu	198
Db	771	TACCAAGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTC	830
Qy	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218
Db	831	AAGCTAGAACTCATAGAGATGATGACATGTAAGTAAGTATACGACGGCTGGG	890
Qy	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238
Db	891	GACACATGCGAGTTCGAACTTCTCTTGGAAATTAACCTCCAGATTCTTGA	950
Qy	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258
Db	951	GGAGAAACAATAGAAATCTGGAAACAGTTATATTTCTGTGATGTTTTCGCC	1010
Qy	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTpsAspGlyArgPhe	278
Db	1011	TTAGGATATTTTGTGTGTGGATGGATGAACCTTATTTGGCACTGGGATGGA	1070
Qy	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297
Db	1071	GATGGAGTGAGCTTTGTAGTTTTCGGTGTGGATGGAAGTCAATTTCTATTC	1130

Qy	298	AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer	317
Db	1131	GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAAACTTGCTTTATG	1190
Qy	318	ArgGlyValGlyAspLysGlySerSerSerHisLenLysProLysAlaThrGlySerThr	337
Db	1191	AGAGTGTGTGGGACAAAGGTTTCAATCCAGTCAATAAACAAGGCTACAGGATCT	1250
Qy	338	SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal	356
Db	1251	TCAGACCTTGGAAATAGAAACAGATCTGAATATTTTATATCCTTAAATGGGTCT	1310
Qy	357	AspSerGlnProGlnSerLysSerLysAsnThrTyrIleAspGluValAlaGluAsp	376
Db	1311	GACTCACACCAACATCCAAATCAAAAATACATGGTACATTTGATGAAGTTGCA	1370
Qy	377	ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln	396
Db	1371	CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCCACCACT	1430
Qy	397	ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu	416
Db	1431	CCTCCTCTGTGAACCTCACTGACCAACGAGAACAGATTCCACTCTTTACCAT	1490
Qy	417	ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln	436
Db	1491	ACCAAGATGCCAATACCAATGGAGATATTGGCCACAGTCCACTTTCTCTGTG	1550
Qy	437	SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro	456
Db	1551	TCTGTAATGGAAGAGCTAAACACTGACCCGCTCCAAAGAGAGTCCACCCCT	1610
Qy	457	ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro	476
Db	1611	CCTGGGAACCTCACATGGTCTAGAAAGTGGGCTCATTTGGCTGAAGTTAAG	1670
Qy	477	PheTyrGlyValIleArgTyrIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly	496
Db	1671	TTCTATGGGTAATCCGTTGGATCGTCCAGCCACCAAGACTGAATGAAGTGTCT	1730
Qy	497	LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr	516
Db	1731	CTGGAACCTGGAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCA	1790
Qy	517	PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer	536
Db	1791	TTACCTGTGCTTGAAGAGGCGCTGTTTGTGAAACTGAAGAGCTGACGAGCT	1850
Qy	537	ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe	556
Db	1851	AGGTTTGCATCATTTGACGCGGTTTCCAAATCAGATTGAGCGCTGTAATCTTT	1910
Qy	557	GlyGlyTyrLeuSerGluValGluGluAsnThrProProLysMetGluLysGluGly	576
Db	1911	GGAGGCTCTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAAG	1970
Qy	577	LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu	596
Db	1971	TTGGAGATAATGATTGGGAAGAAAGGCAATCCAGGCTCATTAATTTCTTTACT	2030
Qy	597	AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg	616
Db	2031	GACTCAACCTTATTTCTGCTTATTTGCTTTTGTAGTCTGTTGGACACTGTGT	2090
Qy	617	ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu	636
Db	2091	CCCAAGAAACACAGATGTAGATAATTTATAGTGAACCCCAAGAGCTACTGAG	2150
Qy	637	IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg	656
Db	2151	ATTGTTAATCTCTGAGAAATATATGATATGTTGTGTGCCCAAAATTTATGA	2210
Qy	657	LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu	676

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Db 2211 AANAATCTTGAAGAGTGGAGCTGCATCAGATTATCTCTGAGAGAAAAGATCCCTGAG 2270
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 2271 GAATCTTGAATATCTGTTTCATCATATTTAAGGTGAGAACCTTTGCTAAAATAAGA 2330
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2331 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAAAAAATGAG 2390
Qy 717 LysValGlyValProThrIleGlnLeuLeuGluTyrPheIleAsnSerAsnLeu 736
Db 2391 AAAGTTGGCGTCCCAAAATTCAGCAGTTGTAGAATGGTCTTTTATCAACAGATAACCTG 2450
Qy 737 LysPheAlaGluAlaProSerCysLeuIleGlnMetProArgPheGlyLysAspPhe 756
Db 2451 AAATTTGAGAGGACCATCATGTCTGATTAATCAGATGCCCTCGATTTGGAAAAGACTTT 2510
Qy 757 LysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeuGluAsp 776
Db 2511 AAATAATTTAAAAAATTTTCTCTCTGGAATTAATAATAACAGATTTACTTGAAGAC 2570
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2571 ACTCCAGACAGTCCCGATATGTGGAGGGCTTGCAATGTATGATGTAGAGAATGCTAC 2630
Qy 797 AspAspProAspIleSerAlaGlyLysIleGlnPheCysLysThrCysAsnThrGln 816
Db 2631 GAGATCCGAGACATCTCAGCTGGAAAAATCAAGCAGTTTGTGTAATCTGCAACACATCA 2690
Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2691 GTCCACCTTCATCCGAGAGGCTGAATCATATAATATAACCCAGTGTCACTTCCCAAGAC 2750
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2751 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTCCCAAGATATGGAGTTATTGCT 2810
Qy 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2811 GTTCTCTGCATAGAAACAACCCACTATGTGCTTTTGTGAAGTATGGGAAGGACGATTCT 2870
Qy 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2871 GCTGGCTCTTCTTTGACAGATGCGCGATGGGATGGTGTGCAATATGGGCTTCAACATT 2930
Qy 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2931 CCTCAAGTCAACCCATGCCAGAGTAGGAGAGTACTTTGAAGATGTCTCTGGAAGACCTG 2990
Qy 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2991 CATTCCTTGACTCCAGAGAAATCCAAAGGCTGTGCACGAGACTGCTTTGTGATGCATAT 3050
Qy 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3051 ATGTGATGTATACCAGAGTCCAAACAATAGTTGTGACAAA 3089
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RESULT 3

US-09-315-788-1729

; Sequence 1729, Application US/09315788

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Holtzman, Douglas A.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

; TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY

; FILE REFERENCE: MLN98-19PM

; CURRENT APPLICATION NUMBER: US/09/315,788

; CURRENT PENDING DATE: 05/05/98

; EARLIER APPLICATION NUMBER: 60/086,455

; EARLIER PENDING DATE: 1998-05-22

; EARLIER APPLICATION NUMBER: 60/132,067

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; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 2346
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1729
; LENGTH: 4664
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4664)
; OTHER INFORMATION: n = A,T,C or G
US-09-315-788-1729
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Alignment Scores:

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Pred. No.: 0 Length: 4664
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservatives: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 23 Gaps: 4
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US-09-671-687A-3 (1-949) x US-09-315-788-1729 (1-4664)

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Qy 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAAGTCACTTCACTCCCTACTGGGAGAGCGGATT 289
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 290 TTTTACTTGTCTTCTTCAAGAAATGCAGCGTTTACAGACAAACAAACAAAGCTCTCTAAA 349
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGAAAGTATAGGACAGTATATTCAGATCGTCTTGTGGGGCATTCAGAGATT 409
Qy 61 ProSerAlaLysGlyLysLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 410 CCTTCTCGAAAGCAAGCAAGAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 469
Qy 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTGTGATGAAAGGATGTTGTAGAGATAAATGAAAGTTTACAGAGTTACTTT 529
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGSCAAATTAACCAATGTGAGAGAGAGGTTACGCTGTTTAAAAACAGAAAAACAGACTAAGT 589
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAAGGCTCCAAATAGACGTGGGCTGCTGTGAAAGTACAGCTGAGATCTGGGGAGAGA 649
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTGGAGTTGATCGCTTCAGAGGACCCCTGTTAGCAGAGAGAGACAGTCTCCGGA 709
Qy 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTCTTGGAGTTGAAATTCCTGSAAGAGAGTCTGTGTCAGAGTTTCACTACGCGGGTG 769
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTCATTTGAC 829
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAGAACTCATAGAAGATGATGACACTGCACTTGGAAAGTATGATGACAGGTCTCTGG 889
Qy 219 AspThrMetGlnValGluLeuProLeuGluLeuAsnSerArgValSerLeuLysGly 238
Db 890 GACACAATGCAAGTTCGAACTTCTCTCTTGGAAATAAACTCCAGAGTTTCTTTGAAGGTT 949
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
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Db 950 GGAGAAACAATAGAACTCGGAACAGTTATATCTGTGATGTTTGGCCAGGAAAAAGAACG 1009
Qy LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1010 TTAGGATATTTTGTGTGTGGACATGGATAAACCTATTGGCAACTGGGATGGAGATTT 1069
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGGAGTCAGCTTTGTAGTTTGGGTGTTGAAAGTAGCAATCTTATTGCACATCAAT 1129
Qy 298 AspileleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTACCCAGAAAGGAGGCTCCCAAACTTGGCTTTATGTCA 1189
Qy 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTGGGGAACAAGGTTCTACGATCATTAATAACCAAGGCTACAGGATCTACC 1249
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTCGAAATAGAAACAGATCTGAATTTATTTATATCTTAAATGGGTCTCTGTT 1309
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCACACCCACCAATCCAAATCAAAATAACATGGTACATTTGATGAAGTTGCAAGAC 1369
Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTACCACCACTCCAG 1429
Qy 397 ProProValAsnSerLeuThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1430 CCTCTCTCTGAACTCACTGACCACCGAGNACAGATTCCACTCTTTACCAATTCAGTCTC 1489
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1490 ACCAAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGACGCCAG 1549
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
Db 1550 TCTGTATGGAAGAGCTAAACACTGCACCCCTCCAGAGAGTCCACCCCTTGGCCATGCCCT 1609
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGAACTCACATGCTAGAGTGGGCTCATTTGGCTGAAGTTAGGAGAACCTCTCT 1669
Qy 477 PheTyrGlyValIleArgTTPileGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 1670 TTCTATGGGGTAATCCGGTTGGATCGGTGAGCCACAGGACTGAATGAAGTCTCGCTGA 1729
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1730 CTGGAACCTGGAAGATGAGTGTGAGGCTGTACGATGGAACCTTTCAGAGGCACTCGGTAT 1789
Qy 517 PheThrCysAlaLeuLeuLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
Db 1790 TTCACTGTGCCCTGAAGAGGCGCTGTTTGTGAACCTGAAGAGCTGCGAGGCTGACTCT 1849
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 1850 AGGTTTGATTCATTCGACCGCGTTTCCAATCAGATTGAGCGCTGTAACCTTTAGCAATTT 1909
Qy 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAGGCTACTTAAAGTAGAGTGAAGAAATACTCCACCAAAATGGAAAAAGAGGC 1969
Qy 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 1970 TTGAGATATGATTTGGGAAGAGAGGCACTCAGGGTCTATTACAATTTCTTTACTTTA 2029
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATCTGCTTATTTGCTTTAGTTCTGTTCTGGACACTGTCTTACTTACA 2089

Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 2090 CCCAAAGAAAGAACGATGTAGATATTTATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2150 ATTGTTAATCTCTGAGAAATATATGGATATGTGTGCGCACAAAAATTTATGAACTGAGG 2209
Qy 657 LysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATACCTTGAAGAGGTGAGGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCCTGAG 2269
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 2270 GAATTCCTGATATCTCTGTTTCATCATATTTTAAGGTAGAACCTTTGCTAAAAATAGA 2329
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGAAAAAATGAG 2389
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2390 AAAGTTGGCGTTCCCAAAATTCAGCAGTTGTAGAAATGGTCTTTTATCAACAGTAACCTG 2449
Qy 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAATTTGCAGAGGCCCATCATGTGATTTATCAGATGCCCTCGATTTGGAAAAAGACTTT 2509
Qy 757 LysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 2510 AAACATTTAAAAAATTTTTCTCTCTGAAATTAATAATAACAGATTACTTCTGAAGAC 2569
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2570 ACTCCAGACAGTCCGGATATGTGGAGGCTTGCAATGTATGATGAGTGTAGAAATGCTAC 2629
Qy 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GACCATCCGGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTGCACACTCAA 2689
Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTTCATCCGAAGAGGCTGAATCATATAATAACCCAGTGTCTCACTTCCCAAAGAC 2749
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2750 TTACCCGACCTGGGACTGGAGACACGGCTGCATCCCTTGCAGAAATATGGAGTTATTTGCT 2809
Qy 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2810 GTTCTCTGCATAGAAACCAAGCCACTATGTTGTTTGTGAAGTATGGGAAGGACCATTTCT 2869
Qy 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2870 GCCTGGCTCTCTTTGACAGCATGGCCGATCGGGATGGTGGTTCAGAAATGGCTTCAACATT 2929
Qy 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTCAACCCATGCCAGAAAGTAGAGACTTGTGAAGATGCTCTGTGAAGACCTG 2989
Qy 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTTGGACTCCAGAGAAATCCAGGCTGTGCACGAAGACTGCTTTGTGATGCATAT 3049
Qy 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGATGTACAGAGTCCAAATAGATTTGTACAAA 3088

RESULT 4

US-09-315-788A-1729

; Sequence 1729, Application US/09315788A

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.
 ; APPLICANT: Holtzman, Douglas A.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
 ; TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY
 ; FILE REFERENCE: 1600.1019-002
 ; CURRENT PUBLICATION NUMBER: US/09/315,788A
 ; CURRENT PUBLICATION DATE: 1999-05-24
 ; PRIOR APPLICATION NUMBER: 09/315,788
 ; PRIOR APPLICATION DATE: 1999-05-24
 ; PRIOR APPLICATION NUMBER: 60/086,455
 ; PRIOR APPLICATION DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/132,067
 ; PRIOR APPLICATION DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 2346
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1729
 ; LENGTH: 4664
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(4664)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-315-788A-1729

Alignment Scores:

Pred. No.: 0 Length: 4664
 Score: 4983.00 Matches: 948
 Percent Similarity: 99.48% Conservative: 0
 Best Local Similarity: 99.48% Mismatches: 1
 Query Match: 98.99% Indels: 4
 DB: 23 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-315-788A-1729 (1-4664)

QY 1 MetSerSerGlyLeuTrpSerGlnGluValThrSerProTyrTrpGluGluArgIle 20
 DB 230 ATGAGTTTCAGGCTTATGAGCCCAAGAAAAGTCACTTCACCTCTACCTGGAAGCGGAT 289
 QY 21 PheTyrLeuLeuGlnGluCysSerValThrAspGlyGlnThrGlnLysLeuLys 40
 DB 290 TTTTACTGCTCTTCAAGAAATGACGCTTACAGACAAACAAACAAAGCTCTTAA 349
 QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
 DB 350 GTACCAAGGGAAGTATAGACAGTATATTCAGATCGTCTCTGTGGGCAATTCAGGAT 409
 QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
 DB 410 CCTTCTGCAAAAGCAAGAAAATCAGATTGGATTAAATAATTCAGAGCAACCTCATGCA 469
 QY 81 ValLeuPheValAspGlu---AspValValGluLysValThrGluLeuLeu 99
 DB 470 GTTCTCTTTGTGATGAAAGGATGTTGTAGATATAATGAAAGTTTCAGAGATTACTT 529
 QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgLeuSer 119
 DB 530 TTGGCAATTTACCAATTTGTGGAGAGGTTTCCAGCTGTTTAAACACAGAACTAAGT 589
 QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
 DB 590 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGAAGTACAGCTGAGATCTGGGGAGAA 649
 QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
 DB 650 AAATTTCTGAGTTGTACGCTTCAGAGGACCTGTTAGCAGAGGACAGTCTCCGGA 709
 QY 160 IlePhePheGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
 DB 710 ATATTCTTTGGAGTTGAATTTGCTGGAGAGGTCGTGGTCAAGGTTTCACTGACGGGGTG 769
 QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198

DB 770 TACCAAGGAAAACAGCTTTTTCAGTGTGATGAAGATTGGCGGTGTTTGTTCATTGGAC 829
 QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
 DB 830 AAGCTAGAACTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACCGCAGTCTCTGG 889
 QY 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
 DB 890 GACCAATGCGAGTCAAGCTTCTCTCTTTGGAAATAAACTCCAGAGTTTCTTTGAAGTT 949
 QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
 DB 950 GGAGAAACAATAGAACTCTGGAACTGATATTCGTGATGTTTTCGCCAGGAAAAGAAC 1009
 QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
 DB 1010 TTAGGATATTTGTTGGTGGACATGATTAACCTATTGGCAACTGGGATGAAGATTT 1069
 QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
 DB 1070 GATGAGTGCAGCTTTGTAGTTTTCGCTGTCTGAAAGTACAAATTCATTTCACATCAAT 1129
 QY 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
 DB 1130 GATATCATCCAGAGGTGTACGCAAGAAAGGAGGCTCCCAAACTTGCCTTTATGTCA 1189
 QY 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
 DB 1190 AGAGTGTGTTGGGCAAAAGGTTTCATCCAGTCAATAATAAACCAAGGCTTACAGATCTAC 1249
 QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
 DB 1250 TCAGACCTCGAAATAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTTCTGT 1309
 QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
 DB 1310 GACTCACACACCAATCCAAATCAAAAATAATACATGTTGATGAAAGTTGCAGAGAC 1369
 QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProLeuGln 396
 DB 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGCTTTTGACCGTCTTCCACCACTCCAG 1429
 QY 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
 DB 1430 CCTCTCTCTGTAACCTCACTGACCACCCAGAACAGATTCCACTCTTTACCATTCAGTCTC 1489
 QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
 DB 1490 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGAGCCAG 1549
 QY 437 SerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
 DB 1550 TCTGTAATGGAAGAGCTTAAACACTGCACCCGCTCCAAAGAGAGTCCACCTTGGCCATGCT 1609
 QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
 DB 1610 CCTGGGAACCTACATGCTTAGAAGTGGCTCATTTGCTGAAGTTAAGAGAACCTCTCT 1669
 QY 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
 DB 1670 TTCTATGGGTAAATCCGTTGGATCGGTGAGTCCAGCCAGGAGTGAATGAAGTCTCGCTGA 1729
 QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
 DB 1730 CTGGAACCTGGAAGATGATGTGAGGCTGTACGAGTGAACCTTTCAGAGGACCTCGGTAT 1789
 QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536
 DB 1790 TTCACCTGTCTGAAAGAGGCGCTGTTGTGAAACTGAAGAGCTGAGGCGCTGACTCT 1849
 QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
 DB 1850 AGTTTGCATCATTTGACGCGGTTTCCAAATCAGATTGAGCGCTGTAACCTTTTAGCATTT 1909

Qy 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAGGCTACTTAAGTGAAGTAGTGAAGAAATACTCCACCAAAATCGAAAAAGAGGC 1969
Qy 577 LeuGluileMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 1970 TTGGAGATAATGATTTGGGAAGAAAGAGGCATCCAGGGTCATTACAATTTCTTTACTTA 2029
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATTCGCTTATTTGCTTTTAGTTCTGTCGACACTGTGTTACTTAGA 2089
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 2090 CCCAAAGAAAGACGATGTAGATATATTAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2150 ATTGTTAATCCTCTGAGATATATGATATGTTGTGTGCCACAAAATTTATGAACTGAGG 2209
Qy 657 LysIleLeuGluLysValGluAlaSerClyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATCTTGAAAGAGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCCTGAG 2269
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 2270 GAATCTTGTAATATCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTTAAAAATAGA 2329
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGAGCTCAAAAGGTACAGATTTTACTTCTATCAAAATTTTATGGAATAAATAGAG 2389
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluThrSerPheIleAsnSerAsnLeu 736
Db 2390 AAAGTTCGCGTTCACCAATTCAGCAGTTGTAGAAATGCTTTTATCAACAGTAACCTG 2449
Qy 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAATTTGCAGAGGACCATCATGCTGATATTATCAGATGCTCGATTTGGAAAGACTTT 2509
Qy 757 LysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 2510 AAACATTTTAAAAAATTTTCTCTCTCGAAATTAATATAACAGATTTACTTTGAAGAC 2569
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2570 ACTCCAGACAGTCCGCGATATGTGAGGGCTTGCATATGTATGATGTAGAGATGTCTAC 2629
Qy 797 AspAspProAspIleSerAlaGlyLysIleGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GAGCATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTGTGTAACCTCGCAACACTCAA 2689
Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTCATCCGAAGGCTGAAATCAATAATATACCAGTGTCTCTCCCAAGAC 2749
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGCCAGATATGAGTATTTGCT 2809
Qy 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2810 GTTCTCTGCATAGAAACAAGCACTATGTTGCTTTTGTGAAGTATGGAAGGACGATTCT 2869
Qy 877 AlaTrpLeuPheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2870 GCCTGGCTCTCTTTGACGATGGCGATGGGATGGTGTGTCAGATGGCTTCAACATT 2929
Qy 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTCAACCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTG 2989

Qy 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTTGGACTCCAGAGAATCCAGGCTGTGCACGAAGACTGCTTTGTATGCATAT 3049
Qy 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGCATGTACCAAGAGTCCAAACAATGAGTTGTACAAA 3088
RESULT 5
US-09-783-514-1729
; Sequence 1729, Application US/09783514
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY
; FILE REFERENCE: 1600.1019-002
; CURRENT APPLICATION NUMBER: US/09/783,514
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 09/315,788
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,455
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/132,067
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 2346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1729
; LENGTH: 4664
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4664)
; OTHER INFORMATION: n = A,T,C or G
US-09-783-514-1729
Alignment Scores:
Pred. No.: 0 Length: 4664
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservatives: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 32 Gaps: 4
US-09-671-687A-3 (1-949) x US-09-783-514-1729 (1-4664)
Qy 1 MetSerSerGlyLeuTyrSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTCAGGCTTATGGAGCCAAAGAAAAGTCACTTCACCTACTGGAGAGCGGATT 289
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 290 TTTTACTTGCTTCTTCAAGATGCGGTTACAGACAAACAAACAAAGCTCCTTAA 349
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGAGGATATAGGACAGTATATCAAGATCGTCTGTGGGCGATTCAAGGATT 409
Qy 61 ProSerAlaLysGlyLysLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 410 CCTTCTGCAAAAGGACAGAAAAATCAGATTGGATTAAAAATCTAGAGCAACCTCATGCA 469
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTTGTTGATGAAAAGGATGTTGTAGAGATAAATGAAAGCTTCACAGATTACTT 529
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTTACCAATTTGTGAGGAGAGGTTTCAGCCCTGTTTAAAAACAGAAACAGACTAAGT 589
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139

Db	590	AAAGGCCTCCAAATAGACGTGGGCTGTCTCTGTGAAGATACAGCTGAGATCTGGGGAAGAA	649
Qy	140	LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly	159
Db	650	AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTGTAGCAGAGAGGACAGTCTCCGGA	709
Qy	160	llePhePheGlyValGluLeuLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal	179
Db	710	ATAATTCTTTGGAGTTGAATTCGTGAAAGAGTCTGTCTCAAGGTTTCACTGACGGGGTG	769
Qy	180	TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp	198
Db	770	TACCAGGGAACAAGCTTTTTCAGTGTGATGAAGATTGTGCGCTGTGTGTTCGATGTGCAC	829
Qy	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218
Db	830	AAGCTAGAACTCATAGAGATGATGACACTGCAATTGGAAAGTATTACGCAGGTCCTGGG	889
Qy	219	AspThrMetGlnValGluLeuProProLeuGluIleLeuSerArgValSerLeuLysGly	239
Db	890	GACACAATTCGAGGTGCAACTTCTCTCTTGGAAATAAACTCCAGAGTTTCTTTCAAGGTT	949
Qy	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258
Db	950	GGAGAACAAATAGAAATCTGGAAACAGTTAATCTGTGATGTTTTTGCAGAGAAAAGAACG	1009
Qy	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe	278
Db	1010	TTAGGATATTTTGTGTGTGTCGACATGGATAACCTATTGGCACTGGGATGGNAGATTT	1069
Qy	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297
Db	1070	GATGGAGTGCAGCTTTGTAGTTTTCGCTGTCTGTAAGTAGTACAAATCTATTGCACATCAAT	1129
Qy	298	AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer	317
Db	1130	GATATCATCTCCAGAGAGTGTACCGAGGAAGAGGCGCTCCCAAACTTGCCCTTTATGTCA	1189
Qy	318	ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr	337
Db	1190	AGAGTGTGTGGGACAAAGTTTCATCCAGTCATATTAACCAAGGGCTACAGNATCTACC	1249
Qy	338	SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal	356
Db	1250	TCAGACCCTCGAAATAGAAAACAGATCTCGAAATATTTTATACCTTTAAATGGCTCTCTGTT	1309
Qy	357	AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp	376
Db	1310	GACTCAACACCACAATCCAAATCAAAAATAATCATGGTACATTTGATGAAGTTGCAGAGAC	1369
Qy	377	ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln	396
Db	1370	CCTGCAAAATCTTTACAGAGATATCTACAGACTTTGACCGTTCCTCACCAACNATCCAG	1429
Qy	397	ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu	416
Db	1430	CCTCCTCTCTGGAATCACTGACCACCAGAACAGATTCCACTCTTTTACCATTCACTCTC	1489
Qy	417	ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln	436
Db	1490	ACCAAGATGCCCAATACAAATGGAAGATTTGGCCACAGTCCACTCTCTCTGTGAGCCAC	1549
Qy	437	SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro	456
Db	1550	TCTGTATGGNAGAGCTTAACACTGCACCCGTCCAGAGAGTCCACCCTTGGCCATGCGCT	1609
Qy	457	ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro	476
Db	1610	CCTGGGAATCACATGTGCTAGAAAGTGGGCTCATTTGGCTGAAGTAAAGGAGAACCCCTCT	1669
Qy	477	PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly	496
Db	1670	TTCTATGGGGTAATCCGTTGGATCGGTCAGCCACCAAGATGAATGAAGTGTCTCGTGGGA	1729

Qy	497	LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr	516
Db	1730	CTGAACTCGAAGATGAGTCGAGGCTGTACGGATGGAACCTTCAGAGCACTCGGTAT	1789
Qy	517	PheThrCysAlaLeuIysIysAlaLeuPheValIysLeuIysSerCysArgProAspSer	536
Db	1790	TTCACTGTGCCCTGAAGAAGGCGCTGTTTGTGAAACTGAAGAGCTGCAGGCCCTGACTCT	1849
Qy	537	ArgPheAlaSerLeuGlnProValSerAsnGlnIleCysArgCysAsnSerLeuAlaPhe	556
Db	1850	AGGTTTGATCATCTTCAGCGCGTTTCATCATGAGTTGAGGCGTGAACCTTTAGCATTTT	1909
Qy	557	GlyGlyTyrLeuSerGluValValGluGluAsnThrProProIysMetGluIysGluGly	576
Db	1910	GGAGGCTACTTAAAGTGAAGTAGTAGAAGAAAACTCCACCAAAATGCAAAAGAAGGC	1969
Qy	577	LeuGluIleMetIleGlyIysIysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu	596
Db	1970	TTGGAGATAATGATGGGAAGAAGAAGCATCCAGGGTCATTACAAATTTCTGTGTACTTA	2029
Qy	597	AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg	616
Db	2030	GACTCAACCTTATCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTGTGTACTTAGA	2089
Qy	617	ProIysGluIysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu	636
Db	2090	CCCAAGAAAGAACGATGTAGATAATATAGTGAACCCAGAGCTACTGAGGACAGAA	2149
Qy	637	IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrIysIleMetIysLeuArg	656
Db	2150	ATTGTTAATCCTCTGAGAATATATGATATGTGTGCCACAAAAATATGAAACTGAGG	2209
Qy	657	LysIleLeuGluIysValGluAlaAspSerGlyPheThrSerGluGluIysAspProGlu	676
Db	2210	AAATACTTTGAAAGGTGGAGGCTGCATCAGGATTTTACCCTCGAAGAAAGATCCTGAG	2269
Qy	677	GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuIysIleArg	696
Db	2270	GAATTCCTTGAATATCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTAAATAAGA	2329
Qy	697	SerAlaGlyGlnIysValGlnAspCysTyrPheTyrGlnIlePheMetGluIysAsnGlu	716
Db	2330	TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAATAAATGAG	2389
Qy	717	LysValGlyValProThrIleGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeu	736
Db	2390	AAAGTTGGCGTTTCCCAATTCAGCAGTTGTTAGAAATGGTCTTTTATCAACAGTAGAACCTG	2449
Qy	737	LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyIysAspPhe	756
Db	2450	AAATTTGCAGAGCACCATCATGTCGTATTATTCAGATGCCTCGATTTGGAAAAAGACTTT	2509
Qy	757	LysLeuPheIysIysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuAsp	776
Db	2510	AAACTATTTAAAAAATTTTCTCTCTCGGAATTAATAATATAACAGATTTTACTTGAAGAC	2569
Qy	777	ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr	796
Db	2570	ACTCCACAGACGTGCCGATATGTGGAGGCTTGCATATGTATGAGTGTAGAGAATGCTAC	2629
Qy	797	AspAspProAspIleSerAlaGlyIysIleLysGlnPheCysLysThrCysAsnThrGln	816
Db	2630	GACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGTTTGTGAAAACTGCAACACTCA	2689
Qy	817	ValHisLeuHisProIysArgLeuAsnHisIysTyrAsnProValSerLeuProIysAsp	836
Db	2690	GTCCACCTTCATCCGAAGAGGCTGAATCATATAATAATATACCCAGTGTCACTTCCCAAGAC	2749
Qy	837	LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla	856
Db	2750	TTACCCGACTGGACTGGAGACACGGCTGCATCCCTTGCAGAAATATGGAGTATTGTCT	2809

QY 437 SerValMetGluGluLeuAenThrAlaProValGlnGlnSerProProLeuAlaMetPro 456
DB 1550 TCTGTAATGAAGAGCTAAACACTGCACCCGCTCCAGAGAGTCCACCCCTTGCCACTGCCT 1609
QY 457 ProGlyAenSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAenProPro 476
DB 1610 CCTGGGAACCTACAATGCTCAGAGTGGGCTCATTTGGCTGAAGTTAAGGGAACCCCTCT 1669
QY 477 PheTyrGlyValIleArgTTPilleGlyGlnProProGlyLeuAenGluValLeuAlaGly 496
DB 1670 TTCTATGGGGTAATCCGTTGGATCGGTGAGCCACAGGACTGAATGAAGTGTCTCGCTGGA 1729
QY 497 LeuGluLeuGluAenGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
DB 1730 CTGGAACCTGAAGATGAGTGTGACGGCTGTACGGATGGAACCTTCAGAGGCCTCGGTAT 1789
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
DB 1790 TTCACCTGTCCCTGAAGAAGGGCTGTTTGTGAACCTGAAGAGCTGACGGCTGACTCT 1849
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
DB 1850 AGGTTTGCATCATGTGACCGCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCAATTT 1909
QY 557 GlyGlyTyrLeuSerGluValValGluGluAenThrProProLysMetGluLysGluGly 576
DB 1910 GGAAGGCTACTTAAGTAGTAGTAGAAGAAATTAATCCACCAAAATGGAAGAAAGGC 1969
QY 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
DB 1970 TTGGAGATTAATGATTGGGAAGAGAAAGGCATCCAGGGTCAATACAACTCTTGTTACTTA 2029
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAenThrValLeuLeuArg 616
DB 2030 GACTCAACCTTATCTGCTTATTTGCTTTAGTTCTGTTCTGGACACTGTGTTACTTGA 2089
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
DB 2090 CCCAAAGAAAGAACCATGTAGAAATATATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
DB 2150 ATTGTTAACTCTGAGATATATAGATATGTGTGTGCCACAAAATTTATGAACCTGAGG 2209
QY 657 LysIleLeuGluLysValGluAlaAaSerGlyPheThrSerGluGluLysAspProGlu 676
DB 2210 AAAATACTTGAAGGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAGATCCTGAG 2269
QY 677 GluPheLeuAenIleLeuPheHisIleLeuArgValGluProLeuLysIleArg 696
DB 2270 GAATCTTGAATATTCTGTTTCATCATATTTAAGGTGAACCTTTGCTAAAAATAAGA 2329
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
DB 2330 TCAGCAGGTCAAGAGTACAAGATTGTTACTTCTATCAAAATTTTATGGAAGAAAATGAG 2389
QY 717 LysValGlyValProThrIleGlnGlnLeuLeuGluThrSerPheIleAenSerAenLeu 736
DB 2390 AAAGTTGGGGTCCCAACAATTCAGCAGTGTGTGAATGGTCTTTTATCAACAGTAACCTG 2449
QY 737 LysPheAlaGluAlaProSerCysLeuIleGlnMetProArgPheGlyLysAspPhe 756
DB 2450 AAATTTGCAGAGGCACCATCATGCTGTGATTAATTCAGATGCTCGATTTGGAAGAACTTT 2509
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAenIleThrAspLeuLeuGluAen 776
DB 2510 AAACATTTAAAAAATTTTCTCTCTCGAATTAATAATAACAGATTTACTTTGAAGAC 2569
QY 777 ThrProArgGlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
DB 2570 ACTCCAGACAGTCCGGATATGTGAGGGCTTGCAATGTATGAGTGTAGAGAATGCTAC 2629

QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAenThrGln 816
DB 2630 GACGATCGGACATCTCAGCTGGAAAAATCAAGCAGATTTGTAAACCTGCAACTCAA 2689
QY 817 ValHisLeuHisProLysArgLeuAenHisLysTyrAsnProValSerLeuProLysAsp 836
DB 2690 GTCCACCTTTCATCCGAAGAGGCTGAATCATAAATATAACCCAGTGTCACTTCCCAAGAC 2749
QY 837 LeuProAspTTPAspTTPArgHisGlyCysIleProCysGlnAenMetGluLeuPheAla 856
DB 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTGCCAGAAATATGGAGTTATTGCT 2809
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspSer 876
DB 2810 GTTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGCAGGATTCT 2869
QY 877 AlaTTPLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAenGlyPheAenIle 896
DB 2870 GCCTGGCTCTTCTTTGACAGCATGCCGATCGGATGGTGGTCAATGGCTTCAACATT 2929
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
DB 2930 CCTCAAGTCAACCCATGCCAGAAAGTAGGAGTACTTTGAAGATGCTCTCTGGAAGACCTG 2989
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
DB 2990 CATCTCTGACTCCAGAGAAATCAAGGCTGTGCACGAAGACTCTTTGTGATGCATAT 3049
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
DB 3050 ATGTGCATGTACCAGAGTCCCAACATGAGTTGTACAAA 3088

RESULT 7

US-09-396-087-4309
; Sequence 4309, Application US/09396087
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: PULMONARY ARTERY SMOOTH MUSCLE LIBRARY
; FILE REFERENCE: MLN98-39PM
; CURRENT APPLICATION NUMBER: US/09/396,087
; CURRENT FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 60/100,260
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 60/107,226
; EARLIER FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 60/131,810
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5220
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4309
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A, T, C or G
US-09-396-087-4309

Alignment Scores:

Pred. No.:	0	Length:	4668
Score:	4903.00	Matches:	948
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	98.99%	Indels:	4
DB:	23	Gaps:	4

US-09-671-687A-3 (1-949) x US-09-396-087-4309 (1-4668)

QY 1 MetSerSerGlyLeuTTPSerGlnGluLysValThrSerProTyrTTPGluGluArgIle 20
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Db 230 ATGAGTTCAGGCTTATGAGCCAAAGAAAAAGTCACTTACCCTACTCGGAGAGCGGATT 289
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 290 TTTTACTTGCTTCTTCAAGAAATGAGCGTTACAGACAAACAAACAGCTCTTTAAA 349
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGGAAGTATAGGACAGTATATTCAAGATCGTTCTGTGGGCGCATTTCAAGGATT 409
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
Db 410 CCTTCTGCAAAAGGCAAGAAAAATCAGATTGGATTAAAAATTCAGAGCAACCTCATGCA 469
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTTGTTGATGAAAGGATGTTGTAGAGATAAATGANAAGTTTCACAGAGTTACTT 529
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTAACCAATTGTGAGGAGAGTTTCAGCCGTGTTTAAAAACAGAAACAGACTAAGT 589
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAAGGCGCTCCAAATAGACGCGGCGTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAAGAA 649
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTCGAGTTGTACCGCTTCAGAGGACCCCTGTTTACAGAGAGGACAGTCTCCGGA 709
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTCTTTGGAGTTGAAATGCTGGAGAGAGTCTGTGTCAGGTTTCACTGACGGGGTG 769
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGGGAAACAGCTTTTTTTCAGTGTGATGAAGATTGTGCGGTGTTTGTTCATTGGAC 829
Qy 199 LysLeuGluLeuIleGluAspAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAAGACTCATAGAAGATGATGACACTGCAATTGGAAAGTATACGCGAGTCTCTGGG 889
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 890 GACACAATGAGGTGCAACTCTCTCTTTGGAAATAAACTCCAGAGTTTCTTTGAAGTT 949
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAGAAACAATAGAACTCGAAACAGATTATTTCTGTGATGTTTTGCCAGGAAAGAAAGC 1009
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1010 TTAGGATATTTTGTGTGTGTGGACATGGATAACCCCTATTGGCAACTGGGATGGAAAGATT 1069
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGGAGTGACGCTTTGTAGTTTTGCGGTGTGTGAAGTACAATCTTATTGGCATTCAAT 1129
Qy 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTGACGAGAAAGAGGCGCTCCCAAACTTGCTTTATGTCA 1189
Qy 318 ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTTGGGACAAAGGTTTCATCCAGTCAATAAATAACCAAGGCTACAGGATCTACC 1249
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTCGGAATAGAAACAGATCGAATATTTTATACCTTAAATGGGTCTCTGTGT 1309
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCACACCAACCAATCCAAATAACAAAAATACATGGTACATTGATGAAGTTGCAGAGAC 1369

Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 1370 CCTGCAAAATCTCTTTACAGAGATATCTACAGACTTTGACCGTCTCTTCCACCACTCCAG 1429
Qy 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1430 CCTCCTCTGTGAACCTCACTGACCACCGAGAACAGATTCCACTCTTTTACCATTCACTCTC 1489
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1490 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTGTGTGCCCCAG 1549
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
Db 1550 TCTGTANTGGAAGAGCTAAACACTGACCCCGTCCAAAGAGAGTCCACCCCTTGGCCATGCT 1609
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGGAACCTCACATGCTTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCT 1669
Qy 477 PheTyrGlyValIleArgTTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 1670 TTCTATGGGTAAATCCGTTGGATCGGTGAGCCACGAGACTGAATGAAGTGTCTCTGGA 1729
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1730 CTGGNACTGGAAGATGAGTGTGACGGCTGTACGGATGGNACCTTCAGAGGCACTCGGTAT 1789
Qy 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
Db 1790 TTCACCTGTGCCCTGAAGAGGCGCTGTTGTGAAACTGAAGAGCTGCAGGCTGACTCT 1849
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 1850 AGGTTTGCATCATTCGACCGCGTTTCCAATCAGATTGAGCGCTGTAACTCTTTTACATTT 1909
Qy 557 GlyGlyTyrLeuSerGluValValGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAGGCTACTTTAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAAGAGGC 1969
Qy 577 LeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 1970 TTGGAGATANTGATTGGGAAGAGAGGATCCAGGGCTATTACAATTTCTTTTACTTA 2029
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATTTCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTGTACTTAGA 2089
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 2090 CCCAAAGAAAGAACGATGTAGAAATATTATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2150 ATTGTTAATCTCTGAGATATATGATATGTGTGTGCCACAAAAATTTATGAACTGAGG 2209
Qy 657 LysIleLeuGluLysValGluAlaAsaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATACTTGAAAGGTGGAGGCTGCATCAGATTACCTCTGGAAGAAAAAGATCCTCGAG 2269
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 2270 GAATTTCTGAATATTTCTGTTTCATCATATTTTAAAGGAGTAAACCTTTGCTAAAAATAA 2329
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGCAGCTCAAAAGGTACAGATTGTGTACTTCTATCAAAATTTTATGGAAAAAATGAG 2389
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2390 AAAGTTGGCGTTCACCAATTCACAGCTGTTTAGAATGGTCTTTTATCAACAGTAACCTG 2449

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QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAATTTGAGAGGACCATCATGTCTGATTAATTCAGATGCCCTCGAATTTGGAAAGACTTTT 2509

QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 2510 AAACATAATTAATAAATTTTCCCTCTCTGGAATTAATAATAACAGATTTACTTGAAGAC 2569

QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2570 ACTCCAGACAGTCCCGGATATGTGGAGGGCTTGCATATGATGATGAGTAGAGATGCTAC 2629

QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGATTTTGTAAACCTGCAACACTCAA 2689

QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTCATCCGAAGAGGCTGATCATTAATAATAATAACCCAGTGTCACTTCCCAAGAC 2749

QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGGCCAGATATGGAGTTATTGCT 2809

QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2810 GTTCTCTGCATAGAAACAAGCCATGTTGCTTTTGTGAAGTAGTGGGAAGGAGCATTTCT 2869

QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2870 GCCTGGCTCTTCTTTGACAGATGGCCGATCGGATGGTGTGAGAAATGGCTTCAACAT 2929

QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTCAACCATCCAGAGAGTAGGAGTACTTGAAGATGTCTCTGSAAGACCTG 2989

QY 917 HisSerLeuAspSerArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTGGACTCCAGGAGAAATCCAAAGGCTGTGCAGAGACTGCTTTGTGATGCATAT 3049

QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGCATGTACCAGAGTCCAAACAATGAGTTGTACAAA 3088
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RESULT 8

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US-09-396-970-7559
; Sequence 7559, Application US/09396970
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: MIXED LYMPHOCYTE LIBRARY
; FILE REFERENCE: MLN98-40PA
; CURRENT APPLICATION NUMBER: US/09/396,970
; CURRENT FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 60/100,293
; EARLIER FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 8756
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 7559
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A,T,C or G
US-09-396-970-7559
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Alignment Scores:

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Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
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```
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 23 Gaps: 4
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US-09-671-687A-3 (1-949) x US-09-396-970-7559 (1-4668)

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QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAAGTCACTTCACTCCCTACTTGGGAAGACGGATT 289

QY 21 PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 230 TTTTACTTGTCTTCTCAAGATTCAGAGCTTACAGACAAACAAACACAAAGCTCCCTTAAA 349

QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGGAAGTATAGGACAGTATATTCAAGATCGTTCTCTGGGGCATTCAGAGATT 409

QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
Db 410 CTTCTGCAAAAGGCAAGAAAATCAGATTGGATTAAAAATTTCTAGAGCAACCTCATGCA 469

QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTGTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCAGAGATTACTT 529

QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTACCAATTTGAGGAGAGGTTACGCTGTTTAAAAACAGAAAACAGACTTAAGT 589

QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAAGSCCTCCAAATAGACGTGGGCTGTCTGTGAAAGTACACGTGAGATCTGGGGAAGAA 649

QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAAATTCCTGGAGTTGTACGCTTTCAGAGGACCCCTGTTTAGCAGAGAGGAGCAGTCTCCGA 709

QY 160 IlePhePheGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTCTTTGAGTTGAAATTCGTGNAAGAGTCTGGTCAAGGTTTCTACTGACGGGGTG 769

QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGGAACACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTCATTGGAC 829

QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAGAACTCATAGAAGATGATGACACTGCAATTGGAAAGTGATTCACGAGGTCCTGGG 889

QY 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 890 GACCAATATGCAAGGTGCAACTTCCCTCTTGGAAATAAACTCCAGAGTTTCTTTTGAAGGTT 949

QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAGAAACAATAGAAATCTGGAAACAGTTATATCTGTGATGTTTCCAGAGAAAAGAACG 1009

QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1010 TTAGGATATTTTGTGTGTGACATGATGAACCTTATTGGCAACTGGGATGGAAGATT 1069

QY 279 AspGlyVal----LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGAGGTGCAGCTTTGTAGTTTTCGCTGTGTGTAAGTACAAATTTCTATTGACATCAAT 1129

QY 298 AspileIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAAACTTGCCCTTATGTCA 1189

QY 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTGGGACAAAGGTTTCATCCAGTCAATAAACCAGGCTACAGAGTCTACC 1249
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QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
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Db 1250 TCAGACCTCGAATAGAAAACAGATCTGAATATATTTATATACCTTTAAATGGGCTCTCTGTT 1309
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QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
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Db 1310 GACTCAACACCAACATCAAAATCAAAATAATCATGGTACATGATGAAGTTGCAAGAGAC 1369
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|
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
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|
|
Db 1370 CCTGCAAAATCTCTTACAGATATCTACAGACTTTGACCGTTCTTACCAACCACTCCAG 1429
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|
QY 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
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|
|
Db 1430 CCTCCTCCTGTGAATCACTGACCAACGAGAACAGATTCACACTCTTTACCAATTCAGTCTC 1489
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|
|
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
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|
|
Db 1490 ACCAAGATGCCCAATACCAATGGAAATTTGGCCACACAGTCCACTTTCTCTGTCAAGCCAG 1549
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|
|
QY 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
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|
|
Db 1550 TCTGTAATGGAAAGCTTAAACACTGCACCCCTCCAAAGAGATCCACCCCTTGGCCATGCCCT 1609
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|
|
QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
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|
|
Db 1610 CCTGGGAACCTCACATGGTCTAGAGTGGGCTCATTTGGCTGAATTAAGGAGAACCTCTCT 1669
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QY 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
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Db 1670 TTCTATGGGGTAAATCCGTTGGATCGGTGAGCCAGCAGACTGAATGAAGTCTCGCTGGA 1729
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QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
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Db 1730 CTGGAACCTGGAAGATAGTGTGAGGCTGTACGGATGGAACCTTTACAGAGGCACCTCGGTAT 1789
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QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
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Db 1790 TTCACTGTGCTTGAAGAGGCGCTGTTGTGAACTGAAGACTGAGAGCCTGACTCT 1849
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QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
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Db 1850 AGGTTTGCATCTTGCAGCGCGTTTCCAAATCAGATTGAGGCTCTGTAATCTTTAGCAATTT 1909
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|
QY 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
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Db 1910 GGAGGCTACTTAAGTGAAGTAGTAGAAGAAAATACTCCACCAAAATGCAAAAGAGGC 1969
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|
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QY 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
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Db 1970 TTGAGATAATGATGGGAAGAAAGAGGATCCAGGGTCAATTAACAATCTTTGTACTTA 2029
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QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerValLeuAspThrValLeuLeuArg 616
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Db 2030 GACTCAACCTTATCTGCTTATTTGCTTTAGTTCTGTTCTGGACACTGTGTACTTAGA 2089
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QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
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Db 2090 CCCAAAGAAAGAACGATGATAGATATATATAGTGAAACCCCAAGAGCTACTGAGGACAGAA 2149
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QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
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Db 2150 ATTTGTTAATCTCTGAGAATATATGGATATGTGTGTCACAAAAATTTATGAACCTGAGG 2209
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QY 657 LysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGlu 676
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Db 2210 AAAATACCTTGAAGAGTGGAGCTGCAATCAGATTTTACCTCTGAAGAAAAGATCCTGAG 2269
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QY 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
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Db 2270 GAATTCCTTGAATATTTCTGTTTCATCATATTTTAAGGGGTAGAACCTTGTCTAAATAAGA 2329
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QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
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Db 2330 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAATAATGAG 2389
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QY 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeu 736
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Db 2390 AAAGTTGGCGTTCACCAATTCAGCAGTGTGTAGAAATGGTCTTTTATCAACAGTAACCTG 2449
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QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
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Db 2450 AAATTTGCAGAGGACCACTCATGCTGATTTATCAGATGCCCTCGATTTGGAAGAGACTTT 2509
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QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
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QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
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|
|
Db 2570 ACTCCAGACAGTCCGATATGTGGAGGCTGCAATGTATGAGTGTAGAGATGCTACTAC 2629
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|
|
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
|
|
|
Db 2630 GACGATCCGGACATCTCAGCTGGAAAATCAAGCAGTTTGTAAAACCTGCAACACTCAA 2689
|
|
|
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
|
|
|
Db 2690 GTCCACCTTTCATCCGAGAGGCTGAATCATATAATAATACCCAGTGTCACTTCCCAAGAC 2749
|
|
|
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
|
|
|
Db 2750 TTATCCGACTGGGACTGGAGACAGGCTGCATCCCTGCCAGAAATATGAGTATTTGCT 2809
|
|
|
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspSer 876
|
|
|
Db 2810 GTTCTCTGCATAGAAAACAGCCACTATGTGCTTTGTGAAGTATGGGAAGGACGATCT 2869
|
|
|
QY 877 AlaTrpLeuPheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
|
|
|
Db 2870 GCCTGGCTCTCTTTGACAGCATGGCCGATCGGATGGTGGTCAAGATGGCTTCAACATT 2929
|
|
|
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
|
|
|
Db 2930 CCTCAAGTCAACCCATGCCAGAGTAGAGAGTACTTGAAGATGCTCTCTGGAAGACCTG 2989
|
|
|
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
|
|
|
Db 2990 CATTCCTTGGACTCCAGAGAAATCCAGGCTGTGCACGAAGACTGCTTTGTGATGCATAT 3049
|
|
|
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
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|
|
Db 3050 ATGTGATGTACAGAGTCCAAACAAATGATTTGTACAAA 3088
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|
|
RESULT 9
US-09-397-424-5019
; Sequence 5019, Application US/09397424
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN OSTEOBLAST LIBRARY
; FILE REFERENCE: MLN98-45PM
; CURRENT APPLICATION NUMBER: US/09/397,424
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,469
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/106,454
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/107,252
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/132,100
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5379
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 5019
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A,T,C or G
US-09-397-424-5019

Alignment Scores:
Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 23 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-397-424-5019 (1-4668)

QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTCAGGCTTATGGAGCCCAAGAAAAGTCACTTCCCTACTCGGGAAGAGCGGATT 289
QY 21 PheTyrIleuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 290 TTTTACTTGTCTTCAAGAAATGAGCGTTTACAGACAAACAAACACAAAGAGCTCTTTAAA 349
QY 41 ValProIleGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCAAGAGGAGATATAGACAGTATATTCAAGATCGTTCTGTGGGCAATTCAAGGATT 409
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAla 80
Db 410 CCTTCTGCAAAAGCAGAAAATACAGATTGGATTAAAAATTTAGAGCAACCTCAATGCA 469
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeu 99
Db 470 GTTCTCTTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTACAGAGTTACTT 529
QY 100 LeuAlaIleThrAsnCysGluLysArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTTACCAATTTGTGAGGAGAGGTTTCAAGCTGTTTAAAAACAGAAAACAGACTAAGT 589
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAAGGCTCCAAATAGACGTGGGCTGTCCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 649
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTGGAGTTGTACGCTTACAGGAGACCCCTGTTAGCAGAGAGGACAGTCTCCGA 709
QY 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTCTTTGGAGTTGAATTTGCTGGAAGAGGCTGCTGGTCAAGGTTTCACTGACGGGGTG 769
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGGAACACAGCTTTTTCAGTGTGATCAAGATTGTGGCGGTGTTGTGATTGGAC 829
QY 199 LysLeuLeuLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AGCTTAGAATCTATAGAGATGATGACATGCAATTGGAAAGTGAATTACGAGGTCCTGGG 889
QY 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 890 GACACAAATGACAGTTCGAATCTCTCTTCTTGGAAATAAATCCAGAGTTCTTTGAAGGTT 949
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAGAAACAATAGAAATCGAAACAGTTATATTCTGTGATGTTTGTCCAGGAAAAAGAGC 1009
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278

1010 TTAGGATATTTTGTGGTGTGGACATGGATTAACCTATTGGCAACTGGGATGGAGATTT 1069
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGAGTGCAGCTTTGTAGTTTTCGCTGTGTTGAAAGTACAAATTTATGGACATCAAT 1129
QY 298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAAACTTGCCTTTATGTCA 1189
QY 318 ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTGGGCAAAAGGTTCTATCCAGTACATAATAAAACCAAGGCTACAGAGTCTACC 1249
QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTCGGAATAGAACAGATCTGAATATTTTATATACCTTAATGGGCTCTCTGT 1309
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCACACCAATCCAAATCAAAATACATGGTACATTGATGAAGTTGCAGAGAC 1369
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTCCACCACTCCAG 1429
QY 397 ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1430 CCTCCTCTGTGAATCACTGACCACCGAGAACAGATTCCACTCTTTTACCATTCAGTCTC 1489
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1490 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGAGCCAG 1549
QY 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
Db 1550 TCTGTAATGGAAGAGCTAAACACTGCACCCCTCAAGAGAGTCCACCTTGGCCATGCGCT 1609
QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGGAACCTCACATGCTTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCT 1669
QY 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 1670 TTTATGCGGTAAATCCGTTGGATCGGTGAGCCACCAAGAGTGAATGAAGTGTCTGCTGA 1729
QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1730 CTGGAACTGGAAAGATGAGTGTGACGGCTGTACGGATGGAACTTCAGAGGCACTCGGTAT 1789
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
Db 1790 TTCACCTGTGCGCTGAAAGAGGCGCTGTTGTGAAACTGAAAGAGCTGAGGCGCTGACTCT 1849
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 1850 AGTTTTCATTCATTCAGCGCGGTTTCCAAATCAGATTGAGCGCTGTAATCTTTAGCATTT 1909
QY 557 GlyGlyTyrLeuSerGluValValGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAGGCTACTTAAGTAGTAGTAGAAGAAATACTCCACCAAAATGAAAAAGAGGC 1969
QY 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrIleu 596
Db 1970 TTGAGATAATGATTGGAAAGAGAGAGGATCCAGGCTCATTAACAATCTTTGTACTTTA 2029
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATTTCTCTTATTTGCTTTTGTGTTTGTCTGAGACACTGTGTACTTGA 2089
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
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Db 2090 CCCAAGAAAGACGATGTAGATATATATAGTGAACCCCAAGAGCTACTGAGACAGAA 2149
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2150 ATTGTTAATCTCTGAGAAATATATGATATGTGTGTCACAAATAATATGAAACTGAGG 2209
Qy 657 LysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATACCTTGAAGAGTGGAGCTGTCATCAGGATTTACCTCTGAAGAAAAGATCCTGAG 2269
Qy 677 GluPheLeuAsnIleLeuPheHisIleuArgValGluProLeuLysIleArg 696
Db 2270 GAATCTTGATATCTGTTTCATCATATTTAAGGTAGAACCTTTGCTTAAATAATAGA 2329
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGCAGCTCAAGGTACAGATGTCTCTATCAATTTTATGGAATAATGAG 2389
Qy 717 LysValGlyValProThrIleGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2390 AAAGTGGCGTTCACAAATTCAGCAGTGTGTAGATGGTCTTTTATCAACAGTAACCTG 2449
Qy 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAATTTTCAGAGGACCATCATGTCTGATTTATTCAGATGCTCGATTTGGAAGACATTT 2509
Qy 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuGluAsp 776
Db 2510 AAATATTTTAAAAATTTTCTCTCTGGAATTAATATAACAGATTTACTTGAAGAC 2569
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2570 ACTCCAGACAGTCCGGATATGTGGAGGCTTCAATGTATGATGTAGAGATGCTAC 2629
Qy 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GAGCATCCGACATCTCAGCTGGAAAAATCAAGCAGTGTGTGTAATACTTCAACACTCAA 2689
Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTCATCCGAAGAGCTCAATCATAAATATAACCCAGTGTCACTTCCCAAGAC 2749
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2750 TTACCCGACTGGAGTGGACACAGCTGCATCCCTTCCAGATATAGGATTTATTTGCT 2809
Qy 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2810 GTTCTCTGCATAGAAACAAAGCCTATGTGTTGTTGTAAGTATGGAAGGACGATTTCT 2869
Qy 877 AlaTrpLeuPheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2870 GCCTGGCTCTCTTTTGACAGCATGCGCATCGGATGTGTGTCAGATGGCTTCAACATT 2929
Qy 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTACCCCATCCCAAGATGAGAGATCTTGAAGATGTCTCTGGAAGACCTG 2989
Qy 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTTGACTCCAGAGAAATCCAGGCTGTGCAGGAAGACTGCTTTGTGATGATAT 3049
Qy 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGTCATGACAGAGTCCAAATGAGTTTGTACAAA 3088

RESULT 10

US-09-397-424A-5019

; Sequence 5019, Application US/09397424A

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

; TITLE OF INVENTION: HUMAN OSTEOBLAST LIBRARY

; FILE REFERENCE: MLN98-45PM

; CURRENT APPLICATION NUMBER: US/09/397.424A

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,469

; PRIOR FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: 60/106,454

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: 60/107,252

; PRIOR FILING DATE: 1998-11-05

; PRIOR APPLICATION NUMBER: 60/132,100

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 5379

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5019

; LENGTH: 4668

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1) - (4668)

; OTHER INFORMATION: n = A,T,C or G

US-09-397-424A-5019

Alignment Scores:

Pred. No.: 0 Length: 4668

Score: 4983.00 Matches: 948

Percent Similarity: 99.48% Conservative: 0

Best Local Similarity: 99.48% Mismatches: 1

Query Match: 98.99% Indels: 4

DB: 23 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-397-424A-5019 (1-4668)

Qy 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20

Db 230 ATGAGTTTCAGGCTTATGAGCCAAAGAAAGTCACTTCACTTCTGGAAGAGCGGATT 289

Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40

Db 290 TTTTACTTGTCTTCTTCAAGAAATGAGCGTTACAGACAAACAAACAAAGCTCTTAA 349

Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60

Db 350 GTACGGAAGGAAGTATAGACAGTATATTCAAGATCGTCTGTGGGCGATTCAGGATT 409

Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80

Db 410 CTTTCTGCAAAAGGCAAGAAATTCAGATTGATTTAAAAATTTCTAGAGCAA CTTCTATGCA 469

Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99

Db 470 GTTCTCTTTGTGTATGAAAGGATGTTTGTAGAGATAAATGAAAGTTTACAGATTACTT 529

Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119

Db 530 TTGCAATTTACCAATTTGTGAGAGAGGTTTCAAGCTGTTTAAAAACAGAAACAGACTT 589

Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139

Db 590 AAAGGCTCCAAATAGACGTGGCTGTCTCTGTGAAAGTACAGCTGAGATCTGGGAAGAA 649

Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159

Db 650 AAATTTCTGAGATTGTACGCTTCAGAGACCCCTGTTTAGCAGAGAGGACAGCTCTCCGA 709

Qy 160 IlePhePheGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal 179

Db 710 ATATTCTTTGGAGTTGAATTTCTGGAAGAGTCTGGTCAAGGTTTCTACGCGGGTG 769

Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198

Db 770 TACCAAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTGTCATTGGAC 829

199 LysLeuGluLeuLeuLeuGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
200 |||||
830 AAGCTAGAACTCAGTAGAAGATGATGACACTGCGATTGGAAAGTGATTACGCGAGTCTCTGGG 889
201 |||||
219 AspThrMetGlnValGluLeuProProLeuGluLeuLeuLeuSerArgValSerLeuLysGly 238
202 |||||
890 GACACAATGCGAGTTCGAACCTTCCTCTTGGAAATAAATCCAGAGTTCTCTTTGAAGGTT 949
203 |||||
239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
204 |||||
950 GGAGAAACAATAGAACTGGAACAGTTATATCTCTGATGTTTGGCAGGAAAGAAAGC 1009
205 |||||
259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
206 |||||
1010 TTAGGATATTTGTTGGTGTGACATGATTAACCTATTGGCAACTGGGATGGAGATT 1069
207 |||||
279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
208 |||||
1070 GATGGAGTGCAGCTTTGTAGTTTGGCTGTGTTGAAAGTACAATTCTATTGCACATCAAT 1129
209 |||||
298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
210 |||||
1130 GATATCATCCAGAGAGTGTGACGACAGAAAGGAGGCTCCCAAACTTGCCTTTATGTCA 1189
211 |||||
318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
212 |||||
1190 AGAGTGTGGGACAAAGGTTCAATCAGTCATAATAAACCAAGGCTACAGGATCTACC 1249
213 |||||
338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
214 |||||
1250 TCAGACCTCGAAATAGAACAGATCTGAATATTTTATACCTTAATGGGCTCTCTGTT 1309
215 |||||
357 AspSerGlnProGlnSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
216 |||||
1310 GACTCACACCAATCCAAATCAAAATACATGTTGATGAAAGTTGCAGAGAC 1369
217 |||||
377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerProProLeuGln 396
218 |||||
1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTCCACCACCTCCAG 1429
219 |||||
397 ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
220 |||||
1430 CCTCTCTCTGTGAACCTACTGACACCGACCGTCCNAGAGAGTCCACCTTGGCCATGCCT 1489
221 |||||
417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
222 |||||
1490 ACCAAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGTGAGCCCG 1549
223 |||||
437 SerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
224 |||||
1550 TCTGTAATGGAAGAGCTAAACACTGACACCGTCCNAGAGAGTCCACCTTGGCCATGCCT 1609
225 |||||
457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
226 |||||
1610 CTGCGAACTCACAATGCTTAGAAGTGGGCTCATTTGGCTGAAAGTAAAGAGAACCCCTCT 1669
227 |||||
477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
228 |||||
1670 TTCTATGGGGTAATCCGTTGGATCGGTGACCCACGAGCTGAATGAAGTGTCTCGCTGGA 1729
229 |||||
497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
230 |||||
1730 CTGGAATGGAAGATGAGTGTGAGGCTGTACCGATGGAACCTTTCAGAGGCACTCGGTAT 1789
231 |||||
517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
232 |||||
1790 TTCACCTGTGCTGGAAGAGCGCTGTTGTGAACCTGGAAGAGTGCAGGCTGACTCT 1849
233 |||||
537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
234 |||||
1850 AGTTTGCATCATTTGCAGCGCGTTTCCAATCAGATTGAGCGCTGTAACCTCTTTAGCATTT 1909
235 |||||

QY 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
D 1910 GGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATAATGAAAAAGAGGC 1969
QY 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
D 1970 TTGAGATAAATGATTGGGAAGAAAGGCATCCAGGGTCATTACAATTTCTTTGTACTTA 2029
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
D 2030 GACTCAACCTTATTCTGCTTATTGCTTTTAGTCTCTGTCGACACTGTGTACTTAGA 2089
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
D 2090 CCCAAAGAAAGAACGATGATAGATATATATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
D 2150 ATTGTTAATCCTCTGAGAAATATATGATATGTTGTGTGTCACAAAAATATGAAACTGAGG 2209
QY 657 LysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGlu 676
D 2210 AAAATATCTTGAAGAGGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCCTGAG 2269
QY 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
D 2270 GAATCTTGAATATCTGTTTCATCATATTTTAGGGTAGAACCTTTGCTAAAAATAAGA 2329
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
D 2330 TCAGCAGGTCAAAAGGTACAGATTTGTACTTCTCTCAATTTTATGGAAAAAATGAG 2389
QY 717 LysValGlyValProThrIleGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
D 2390 AAAGTTGGCGTCCCAAAATTCAGCAGTTGTTAGATGGTCTTTTATCAACAGTAGTAACCTG 2449
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
D 2450 AAATTTGCAGAGGCACCATCATGTCTGATATTTCAGATSCCTCGATTTGGAAAAAGACTTT 2509
QY 757 LysLeuPheLysIlePheProSerLeuLeuLeuAsnIleThrAspLeuLeuGluAsp 776
D 2510 AAATATTTAAAAAAATTTTCTCTCTGGAATTAATAATAACAGATTTACTTGAAGAC 2569
QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
D 2570 ACTCCAGACAGTCCCGGATATGTGGAGGCTTGCATGTATGATGATGAGTAGAAGTGTAC 2629
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
D 2630 GACGATCCGGACATCTCAGCTGGAAAAAATCAAGCAGTTTTTTGAAACCTGCAACACTCAA 2689
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
D 2690 GTCCACCTTCATCCGAAGAGCTGAATCATATAATATCAACCCAGTGTCTACTTCCCAAGAC 2749
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
D 2750 TTACCCGACTGGGACTCGAGACAGCGCTGCATCCTTGGCCAGAAATATGGAGTTATTGCT 2809
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
D 2810 GTTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTAGTAGGAAGACAGATTCT 2869
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
D 2870 GCCTGGCTCTCTTTGACAGCATGCGCGATCGGGATGGTGTGTCAGATGGCTTCAACATT 2929
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
D 2930 CCTCAAGTCACTCCCATGCCAAGAGTAGGAGACTTTGAAGATGTCTCTTGGAGACCTG 2989
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936

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Db 2990 CATTCCTGGAGCTCCAGGAGAAATCCAGGCTGTGCACGAAAGCTGCTTTGTGATGCATAT 3049
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGCATGTACACAGAGTCCAAACAATGAGTTGTACAAA 3088

RESULT 11
US-09-432-241A-3760
; Sequence 3760, Application US/094322241A
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN EPIDERMAL KERATINOCYTE LIBRARY
; FILE REFERENCE: 1600.1004001
; CURRENT APPLICATION NUMBER: US/09/432,241A
; CURRENT FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/106,445
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/107,227
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/127,182
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,099
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5041
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3760
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A, T, C or G
US-09-432-241A-3760

Alignment Scores:
Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 24 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-432-241A-3760 (1-4668)
QY 1 MetSerSerGlyLeuTyrSerGlnGluValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTTCAGGCTTATGGAGCCAGAAAGAAAGTCACTTCACCTTACTGGGAGAGCGGATT 289
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 290 TTTTACTTCTCTTCAAGATGCAGCGTTACAGACAAACAAACAAAGCTCTCTTAAA 349
QY 41 ValProLysGlySerIleGlnTyrIleClnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGGAAGTATAGGACAGATATATTCAGATCGTTCTGTGGGGCATTCAGAGATT 409
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
Db 410 CCTTCTGCAAAAGGCAAGAAAGAAATTCAGATTGGATTAAAAATTCAGAGCAACCTCATGCA 469
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTGTGTAAGAGGATGTTGTAGAGTAATGAAAGTTTACAGAGTTACTT 529
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTACCAATTGTGAGGAGGTTTCAGCGCTGTTTAAAAACAGAAACAGACTAAGT 589
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
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Db 590 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGAAGTACAGCTGAGATCTGGGGAAGAA 649
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTGTGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGGACAGCTCTCCGGA 709
QY 160 IlePhePheGlyValGluLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATCTTTGGAGTTGAATGCTGGAAGAGGTGCTGCTCAAGGTTTCTACTACCGGGGTG 769
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGAAACACAGCTTTTTCAGTGTGATGATGCGGCTGTTGTTGTCATTCGAC 829
QY 199 LysLeuGluLeuIleGluAspAspThrValIlePheCysAspValLeuProGlyLysGluSer 218
Db 830 AAGCTAGAACTCATAGAAGATGATGACATCTGTAAGAGTGTATTCAGCAGGTCTCTGG 889
QY 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 890 GACAAATGCAGGTGCAACTTCTCTTGGAAATAAACTCCAGAGTTCTTTGAAGGTT 949
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAGAAACAATAGAAATCTGGAACAGTTATATCTGTGATGTTTGGCCAGGAAAGAAAGC 1009
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1010 TTAGGATATTTGTTGGTGTGGACATGATGATACCTATTGGCAACTGGGATGGAAGATT 1069
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGAGTGCAGCTTTGTAGTTTTCGCGTGTGTGAAGTACAATTCATATGACATCAAT 1129
QY 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTGACGAGGAAGAGGCTCCCAAACTTGCCTTTATGTCA 1189
QY 318 ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTGGGGACAAAGGTTTCATCCAGTCAATAAACAAGGCTTACAGGATCTACC 1249
QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTCGAAATAGAAAACAGATCTGAATATATTTATACCTTAAATGGGCTCTCTGTT 1309
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCACACACCAACATCCAAATCAAAAATACATGTTACATGTAAGATTGCAAGAGAC 1369
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProLeuGln 396
Db 1370 CCTGCAAAATCTCTTTACAGAGATATTCAGACATTTGACCGTTCCTTACCACCATCCAG 1429
QY 397 ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1430 CCTCCTCTGTGAATCACTGACCAACAGAGAGATTTCCCACTCTTTTACCATTCAGTCTC 1489
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1490 ACCAAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGACCCAG 1549
QY 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
Db 1550 TCTGTATGGAAGAGCTAAACACTGCACCGTCCAGAGAGATCCACCTTGGCCATGCCT 1609
QY 457 ProGlyAsnSerHisGlyLeuGluValIleGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGGAACCTCACATGCTGTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGAGAACCTCTCT 1669
QY 477 PheTyrGlyValIleArgTrpIleGlyClnProProGlyLeuAsnGluValLeuAlaGly 496
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Db 1670 TTCTATGGGGTAATCCGTTGGATCGGTACGCCACCAGGACTGAATGAAGTGGCTCGCTGGA 1729
QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1730 CTGGAACCTGGAAGATGAGTGTGCGAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTAT 1789
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536
Db 1790 TTCACTGTGCCCTGAAGAAGGCGCTGTTGTGAACTGAAGAGCTGCAGGCCCTGACTCT 1849
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 1850 AGGTTTGCACTATGCGCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCAATT 1909
QY 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAAGAGGC 1969
QY 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 1970 TTGGAGATAATGATTGGGAAGAAAGGCAATCCAGGGCTCAATACAAATCTTGTACTTA 2029
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATCTGCTTATTTGCTTTAGTTCTGTTCTGGACACTGTGTACTTAGA 2089
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 2090 CCCAAAGAAAAGAACGATGAGAAATATATAGTGAACCCCAAGACTACTGAGACAGAA 2149
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2150 ATTGTTAATCCTCGAATATATATGATATGTGTGCCACAAAAATTTATGAACCTGAGG 2209
QY 657 LysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATCTTTGAAAGGTGGAGGCTGCATCAGGATTTACCTCTCAAGAAAAAGATCCTGAG 2269
QY 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLysIleArg 696
Db 2270 GAATCTTGAAATATCTGTTTCATCATATTTTAAAGGGTAGAAGCTTTGCTAAAAATAGA 2329
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAATAAATGAG 2389
QY 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeu 736
Db 2390 AAAAGTTGGCGTTCCCAATTCAGCAGTTGTTAGAATGGTCTTTTATCAACAGTAACCTG 2449
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAATTTGCAGAGGCACCATCATGCTCGATTATTCAGATGCTCGATTGGAAGAACTTT 2509
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 2510 AAACATATTAAAAAATTTTCTCTCTGGAATTAATAATACAGATTTACTTTGAGAC 2569
QY 777 ThrProArgGlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2570 ACTCCAGACAGTCCCGGATATGTGAGGCGCTTGCAATGTATGAGTGTAGAGAATGCTAC 2629
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTGCAACACTCAA 2689
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTCATCCGAAGAGGCTGAATCATATAATATAACCCAGTGTCACTTCCCAAGAC 2749
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2750 TTACCCGACTGGGACTGGAGACAGCGCTGCATCCCTTGCAGAAATATGAGATTATTGTCT 2809

QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2810 GTTCTCTGCATAGAAAACAAGCCACTATGTTCTTTGTGAAGTATGGGAAGCAGCATTTCT 2869
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2870 GCCTGGCTCTTCTTTGACAGCATCGCCGATCGGATGGTGTGATGGCTTTCAACATT 2929
QY 897 ProGlnValThrProCysProGluValGlyGlyTyrLeuLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTCAACCCATGCCCAGAAAGTAGGAGAGTACTTTGAAGATGCTCTCTGGAAGACCTG 2989
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTTGGACTCCAGAGAAATCCAAGGCTGTGCAGAAAGACTGCTTTGTGATGCATAT 3049
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGCATGTACCAGATGCCAACAAATGAGTTGTACAAA 3088

RESULT 12

US-09-434-737-1278
; Sequence 1278, Application US/09434737
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN MIXED LYMPHOCYTE LIBRARY
; FILE REFERENCE: 1600.1067001
; CURRENT APPLICATION NUMBER: US/09/434, 737
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: 60/107,228
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 1830
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1278
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A,T,C or G
US-09-434-737-1278

Alignment Scores:
Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 24 Gaps: 4

US-09-671-687A-3.(1-949) x US-09-434-737-1278 (1-4668)

QY 1 MetSerSerClyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTGAGGCTTATGGAGCCCAAGAAAAAGTCACTTCCCTACTGGGAAGCGGATT 289
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 290 TTTTACTTGTCTTCAAGNATCGAGGTTACAGACAAACAAACAAAGCTCTTAAA 349
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCAGAGGGAAGTAGGACAGTATATTCAAGATCGTTCTGTGGGCGATTCAAGGATT 409
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 410 CCTTCTGCAAAAGGCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 469
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99

Db 470 GTTCTCTTCTGATGATAAAGGATGTTGTAGAGATAAATAAGTTCACAGAGTTACTT 529
Qy 100 LeuAlaIleThrAsnCysGluGluAArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTAACCAATGTGTAGGAGAGGTTTCAAGCCTGTTTAAAAACAGAAAACAGACTAAGT 589
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAAGGCTCCAAATAGACGTGGGCTGCTGTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 649
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTGTAGCAGAGAGCAGACTCCCGGA 709
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTTCTTGGAGTTGAATTTGCTGGAAAGAGGTGCTGGTCAAGGTTTTCACGTGACGGGGTG 769
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGAAACAGCTTTTTCAGTGTGATGAGATTTGTGGCTGTTTGTTCATTTGGAC 829
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAGAACTCATAGAAAGATGATGACACTGCATTGGAAAGTGAATACGCAGGTCCTGGG 889
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 890 GACACAAATGAGGTGCAACTTCCTCTTTGGAAATAAACTCCAGATTTCTTTGAAGGTT 949
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAAACAATAAGATCTGGAACAGTTATATTCTGTGATGTTTTCAGCAAGAAAGAAAGC 1009
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1010 TTAGGATATTTTGTGTGTGGACATGATGATAACCTATTGGCAACTGGGATGGAAGATT 1069
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGGAGTGAGCTTTGTAGTTTGTGCTGTTGAAAGTCAAAATCTTATTTGCACATCAAT 1129
Qy 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGGTGACGACGAAAGAGGCTCCCAAACTTGCTTTATGTCA 1189
Qy 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTTGGGACAAAGGTTCAATCCAGTCATATATAAACCNAAGGCTACAGGATCTACC 1249
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTGGAAATAGAAAACAGATCTGAATATTTTATACCTTAAATGGGTCTTCTGTT 1309
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCAACCAACCAATCAAAATCAAAATATACATGATGATGATGATGATGATGATGATGAT 1369
Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTCAGCCGTTCTTCCACCACTCCAG 1429
Qy 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1430 CCTCTCTCTGTGAATCTCACTGACCAACGAGACAGATTTCCACTCTTTTACCATTCAGTCTC 1489
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1490 ACCAAGATGCCCAATACCAATGGAAGATTTGGCCACAGTCCACTTTCTCTGTGAGCCCGAG 1549
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456

Db 1550 TCTGTAATGGAAGAGCTAAACACACTGCACCCCTCCACAGAGAGTCCACCCCTTGCCCATGCT 1609
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGGAACATCACATGTGTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCT 1669
Qy 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 1670 TTCTATGGGGTAAATCCGTTGGATCGGTGAGCCACAGGACTGAATGAAGTGTCTCGTGA 1729
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1730 CTGAACTGGAAGATGAGTGTGAGGCTGTACGGATGGAACCTTTCAGAGGCACTCGGTAT 1789
Qy 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536
Db 1790 TTCACCTGTGCCCTGGAAGAGGCGCTGTTGTGAAACTGAAAGAGCTGCAGGCGCTCACTCT 1849
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 1850 AGTTTTCATCATTTGAGCCGTTTCCAATCAGATTGAGCGCTGTAATCTCTTACATTT 1909
Qy 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAGGCTACTTAACTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAGAAAGAGC 1969
Qy 577 LeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 1970 TTGGAGATAATGATTGGGAAGAAAGAGGATCCAGGCTCATTAACAATTTCTTGTACTTA 2029
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATTTCTCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTGTTACTTAA 2089
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 2090 CCCAAAGAAAGAACGATGTAGATAATTATAGTCAAAACCCCAAGAGCTACTGAGGACAGAA 2149
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2150 ATTGTTAATCTCTGAGAATATATGATATGTGTGTGCCCAAAATTTATGAACTGAGG 2209
Qy 657 LysIleLeuGluLysValGluAlaAspGlyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATCTTGAAGAGGTGGAGGCTGCATCAGATTACCTCTGAAGAAAGATAGATCTGAG 2269
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLysIleArg 696
Db 2270 GAATTTCTTGAATATTTCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTTAAAAATA 2329
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGCAGCTCAAAAGGTACAAAGATTGTTCTTCTATCAAAATTTTATGGAAAAAATAG 2389
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuTrpSerPheIleAsnSerAsnLeu 736
Db 2390 AAAGTTGGCGTTCACAAATTCAGCAGTGTGTAGAAATGATGATGATGATGATGATGATGAT 2449
Qy 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAATTTGCAGAGGACCATCATGCTCATTTATTCAGATGCTCGATTTGGAAAAAGACTTT 2509
Qy 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 2510 AAACATATTTAAAAAATTTTCTCTCTCTGGAATATAATAAATGATGATGATGATGATGATGAT 2569
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGlyCysTyr 796
Db 2570 ACTCCCAAGACAGTCCGGAATATGGAGGGGCTTCAATGATGATGATGATGATGATGATGAT 2629
Qy 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GACGATCCGGACATCTCAGCTGGGAAATCAAGCAGTTTCTGTAACACCTGCAACTCA 2689

QY 817 ValHisLeuHisProLysArgLeuAenHisLysTyrAenProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTCATCCGAAGAGCTGAATCATAAATAAACCAGTGTCACTTCCCAAGAC 2749
QY 837 LeuProAspTrpAspTrpArgHisGlyCysLeuProCysGlnAenMetGluLeuPheAla 856
Db 2750 TTACCCGACTGGGACTGGAGACCGCTGCATCCCTTGCAGAAATATGGAGTTATTGCT 2809
QY 857 ValLeuCysLeuGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2810 GTTCTCTGCATAGAAACAAGCCCATATGTTGCTTTTGTGAAGTATGGAGGACGATTCT 2869
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAenGlyPheAenIle 896
Db 2870 GCCTGGCTCTTCTTTGACAGCATGCCGATCGGATGGTGTGCAAGATGCTCTCTGGAAGACCTG 2929
QY 897 ProGlnValThrProCysProGluValGlyGluThrLeuLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTCAACCCATGCCAGAAAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTG 2989
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTTGGACTCCAGGAGATCCAAAGCTGTGCAAGAGACTGCTTTGTGATGCATAT 3049
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGCATGTACACAGACTCCCAACAATGAGTTGTACAAA 3088

RESULT 13

US-09-850-118-1278
; Sequence 1278, Application US/09805118
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; HUMAN MIXED LYMPHOCYTE LIBRARY
; FILE REFERENCE: 1600.1067-002
; CURRENT APPLICATION NUMBER: US/09/850.118
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/107,228
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 09/434,737
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 1830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1278
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A,T,C or G
US-09-850-118-1278

Alignment Scores:
Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 33 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-850-118-1278 (1-4668)

QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAAGTCACTTCCACCTACTGGGAAAGCGGATT 289
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 290 TTTTACTTGTCTTCTTCAAGNATGACGGTTACAGACAAACAAACAAAAGCTCCTTTAA 349

QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGGAAGTATAGGACAGTATATTCAAGATCGTTCTGTGGGGCATTCAAGGATT 409
QY 61 ProSerAlaLysGlyLysLeuAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 410 CCTTCTGCAAAAGGCAAGAAAAATCAGATTGGATTAAAAAATTTCTAGAGCAACCTCATGCA 469
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTTGTGATGAAAGAGTGTGTAGAGATAAATGAAGTTTACAGAGTTTACTT 529
QY 100 LeuAlaIleThrAenCysGluGluArgPheSerLeuPheLysAenArgAsnArgLeuSer 119
Db 530 TTGGCAATTACCAATTGTGAGGAGAGGTTTCAGCCTGTTTAAAAACAGAAACAGACTAAGT 589
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAAGCCCTCCAAATAGACGTGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 649
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTGAGTTGTACGCTTCAGAGGACCCCTGTGTAGCAGAGGACAGTCTCCGGA 709
QY 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTCTTTGGAGTTGAATTCTGGAAGAGGTCGTGTCGTCGTCGTCGTCGTCGTCGTCG 769
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGGAACAGCTTTTTCAGTGTGATCAAGATTCTGCGCTGTTTGTTCATTGGAC 829
QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAGAACCTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACGACAGTCTCGG 889
QY 219 AspThrMetGlnValGluLeuProLeuGluLeuAenSerArgValSerLeuLysGly 238
Db 890 GACAAATGCAAGTCGAACTTCTCTTTGAAATAAATCCAGAGTTTCTTTGAAGTT 949
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAGAAACAATAGAAATCTGGAACAGTTATATTCTGTGATGTTTGTCCAGGAAAGAAAGC 1009
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProLleGlyAsnTrpAspGlyArgPhe 278
Db 1010 TTAGGATATTTTGTGTGGTGGACATGATGAACCTATTGGCAACTGGGATGGAAGATTT 1069
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGGAGTCAGCTTTTGTAGTTTTCGCTGTGTTGAAAGTACAATTTCTATTGACATCAAT 1129
QY 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAAACTTGCCTTTATGTCA 1189
QY 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTGGGACAAAGGTTTCATCCAGTCATAATAAACCAAGGCTACAGGATCTACC 1249
QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTCGAAATAGAAAACAGATCTGAATTAATTTATACCTTAAATGGGCTCTCTGT 1309
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCACCAACCAATCCAAATCAAAAAATACATGGTACATTGATGAAGTTGCAAGAGAC 1369
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGCTTCTTCCACCACCTCCAG 1429

Db 1585 ATGAGTTACGGCTATGAGCCCAAGAAAAAGTCACTTCCCTACTCGGGAAGACGGGATT 1644
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 1645 TTTTACTTGCTTCTTCAAGAATGAGGTTACAGACAAACAAACACAAAGCTCTTAAA 1704
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 1705 GTACCGAAGGAAAGTAGTAGACAGTATATTCAAGATCGTTCTGTGGGCGATTCAAGGATT 1764
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAla 80
Db 1765 CCTTCTGCAAAAGCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 1824
Qy 81 ValLeuPheValAspGlu---AspValValClnIleAsnGlnLysPheThrGluLeuLeu 99
Db 1825 GTTCTCTTTGTCATGAAGAGGATGTTGTAGAGATAAATGAAAGTTTACAGAGTTACTT 1884
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 1885 TTGGCAATTAACCAATTGTGAGGAGAGGTTGAGCTGTTTAAAAACAGAAACAGACTAAGT 1944
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 1945 AAGGCTCCAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 2004
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 2005 AATTTTCTTGAGTTGTACGCTTCAGAGGACCCCTGTTTACAGAGAGCAGCTCTCCGGA 2064
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 2065 ATATTCTTTGGAGTTGAAATGCTGGAAGAGGTCGTGCTCAAGGTTTCACTGACGGGGTG 2124
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 2125 TACCAAGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTGCAATTGGAC 2184
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 2185 AAGCTAGAACTCATAGAAGATGATGACCTGCAATGGAAAGTATTACCGCAGGTCTCTGGG 2244
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 2245 GACACAAATCGAGTGCACCTCTCTCTTGGAAATAAATCCACAGATTCTTTGAAGGTT 2304
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 2305 GGAGAAACAATAAGAACTGGAACAGTTATATTCTGTGATGTTTGGCAGGAAAGAAAGC 2364
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 2365 TTAGGATATTTGTTGGTGTGGACATGGATTAACCTATTGGCAACTGGGATGAAGATT 2424
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 2425 GATGGAGTCAGCTTTGTAGTTTGGCTGTGTTGAAAGTACAATTCTATTGGACATCAAT 2484
Qy 298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
Db 2485 GATATCATCCAGAGAGTGTGACGCAAGAAAGAGGACCTCCCAAACTTGCTTTATGTCA 2544
Qy 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysPheProLysAlaThrGlySerThr 337
Db 2545 AGAGGTGTTGGGCAACAAAGGTTTCATCCAGTCATAATAAACCAAGGCTACAGGATCTACC 2604
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 2605 TCAGACCTCGGAATAGAAACAGATCTGAATTATTTTATACCTTAAATGGGCTCTCTGTT 2664
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 2665 GACTCACACCAACCAATCCAAATCAAAAAATACATGGTACATTGATGAAGTTGCAGAGAC 2724

Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 2725 CCTCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTCTTCCACCACCATCCAG 2784
Qy 397 ProProProValAsnSerLeuThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 2785 CCTCCTCTGTGAACCTCACTGACCACCGAAGACAGATTCCACTCTTTTACCATTCAGTCTC 2844
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerLeuAlaGln 436
Db 2845 ACCAAGATGCCAATATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGACGCCAG 2904
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGlnGluSerProProLeuAlaMetPro 456
Db 2905 TCTGTAAATGGAAGAGCTAAACACTGACCCCGTCCAGAGAGTCCACCCCTTGGCCATGCCT 2964
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 2965 CCTGGAACTCACATGCTTAGAAGTGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCT 3024
Qy 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 3025 TTCTATGGGGTAATCCGTTGGATCGGTGAGCCACAGGACTGAATGAAGTGTCTCGCTGA 3084
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 3085 CTGGAATCTGAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTAT 3144
Qy 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
Db 3145 TTCACCTGTGCCCTGAAGAGGCGCTGTTTGTGAACCTGAAGAGCTGCAGGCTGACTCT 3204
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 3205 AGGTTTGCATCAATTGACGCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATTT 3264
Qy 557 GlyGlyTyrLeuSerGluValValGluAsnThrProProLysMetGluLysGluGly 576
Db 3265 GGAAGGCTACTTAAAGTAGTAGAAGAAATAACTCCACCAAAATCGAAAAAGAGGC 3324
Qy 577 LeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 3325 TTGGAGATATGATTGGGAAGAAAGAGGCATCCAGGGTCAATTACAATCTTGTACTTA 3384
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 3385 GACTCAACCTTATTCTGCTTATTGCTTTTAGTTTCTGTTCTGGACACTGTGTACTTGA 3444
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 3445 CCCAAAAAGAAAGAACGATGTAGAATAATTATAGTGAACCCCAAGAGCTACTGAGGACAG 3504
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 3505 ATTGTTAATCCTCTGAGAATATATGGATATGTGTGTGCCCAAAAAATTTATGAACCTGAGG 3564
Qy 657 LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 3565 AANAATCTTGAAGGTTGGAGGCTGCATCAGGATTTTACCTCTGAAGAAAAAGATCTCTGAG 3624
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 3625 GAATCTTGAATATCTGTTTTCATCATATTTAAGGGTAGAACCTTTTGTCTAAAAATAAGA 3684
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 3685 TCAGCAGGTCAAAAGGTACAAAGATTGTTACTTCTATCAAAATTTTATGGAAAAAATGAG 3744
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 3745 AAAGTTGGCGCTTCCCAAAATTCAGCAGTTGTAGATGGTCTTTTATCAACAGTAACCTG 3804

Db 2605 TCAGACCTCGAATAGAAACAGATCTGAATTTATTTATACCTTAATGGGTCTTCTGTT 2664
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 2665 GACTCACAACCAATCCAAATCAAAATACATGTTGATGAAAGTTCAGAGAAC 2724
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerProLeuGln 396
Db 2725 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCCACCACCACTCCAG 2784
QY 397 ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 2785 CCTCTCTGTGAACCTCACTGACACCCGAGAACAGATTCACCTCTTTACCACTTACGCTC 2844
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 2845 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGAGCCAG 2904
QY 437 SerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProLeuAlaMetPro 456
Db 2905 TCTGTATGGAAGAGCTAAACACTGCACCCGTCGAGAGAGTCCACCCCTTGGCCATGCCT 2964
QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 2965 CTTGGGAACCTCACTGCTAGAAAGTGGCTCATTTGGCTGAAGTTAAGGAGAACCCCTCT 3024
QY 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 3025 TTCTATGGGTAACTCCGTGGATCGGTGAGCCACAGGACTGANTGAAGTCTCGCTGGA 3084
QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 3085 CTGGAACCTGGAAGATGAGTGTGAGGCTGTACGATGGAACCTTCAGAGGCACTCGGTAT 3144
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536
Db 3145 TTCACCTGTGCCCTGAAGAGGCGCTGTTGTGAACCTGAGAGCTGCAGGCTGACTCT 3204
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 3205 AGTGTTCATCANTGACGCGGTTTCCATCAGATTGAGCGCTGTAATCTTTAGCAATTT 3264
QY 557 GlyGlyTyrLeuSerGluValValGluLeuAsnThrProProLysMetGluLysGluGly 576
Db 3265 GGAGGCTACTTAAGTGAAGTAGTAGAAGAAATATCTCCACCAAAATGGAAGAGGAGGC 3324
QY 577 LeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 3325 TTGGAGATATGATTGGGAAGAGAAAGGCATCCAGGGTCAATTACAAATCTTGTACTTA 3384
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 3385 GACTCAACCTTATTCTGCTTATTGCTTTTGTAGTTCTGTTCTGACACTGTGTACTTAGA 3444
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 3445 CCACAAAGAAAGAACGATGAGATATATAGTGAACCCAGAGCTACTGAGACAGAA 3504
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 3505 ATGTGTTAATCCTCTGAGATATATGATATGTGTGTGCCACAAAATATGAACTGAGG 3564
QY 657 LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 3565 AAAATACTTGAAGAGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCTCTGAG 3624
QY 677 GluPheLeuAsnIleLeuPheHisHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 3625 GAATCTTGAATATCTCTGTTTCATCATATTTAAGGGTAGAACCTTTGTCTAAAATAAGA 3684
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 3685 TCAGCAGGTCAAAAGGTACAGATTGTTACTTCTATCAATTTTTTATGGAAAAAATGAG 3744

QY 717 LysValGlyValProThrIleGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeu 736
Db 3745 AAAGTTGGCTTCCCACAATTGAGAGTTGTTAGAAATGCTCTTTATCAACGTAACCTG 3804
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 3805 AAAATTGGCAGAGGCACCATCATGTCTGATTTATTCAGATGCCCTCGATTTGGAAGAACTTT 3864
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 3865 AAACCTATTTAAAAAATTTTCTCTCTGGAATTAATATATACAGATTTTACTTGAAGAC 3924
QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 3925 ACTCCACAGAGTGGCGGATATGTGAGGGCTTGCATATGATGATGATGAGTATGAGAACTCTAC 3984
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 3985 GACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTGCAACCTCAA 4044
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 4045 GTCCACCTTTCGAGAGGCTGANTCATTAATATAACCCAGTGTCACTTCCCAAGAC 4104
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 4105 TTACCCGAGCTGGAGCTGGAGACACGGCTGCATCCCTGCCAGAAATATGGAGTTATTGCT 4164
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 4165 GTTCTCTGCATAGAAACAAGCCACTATGTTGTTGTGAAGTATGGGAAGGACGATTCT 4224
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 4225 GCCTGGCTCTTCTTTGACAGCATGCCATCGGGATGGTGTGAGAAATGGCTTCAACATT 4284
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 4285 CCTCAAGTCAACCCATGCCAGAGAGTAGAGAGTACTTTGAAGATGTCTCTGGAAGACCTG 4344
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 4345 CATTCCTTGGACTCCAGAGAAATCAAGGCTGTGCACGAGACTGCTTTGTGATGCATAT 4404
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 4405 ATGTGCATGTACCAGAGTCCAAACAATGAGTTGTACAAA 4443

RESULT 16

US-10-170-235-39761
; Sequence 39761, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: C0001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 39761
; LENGTH: 6871
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-39761

Alignment Scores:
Pred. No.: 0 Length: 6871
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 42 Gaps: 4

QY 717 LysValGlyValProThrIleGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2438 AAAGTTGGCGTTCCTCCAAATTCAGCAGTTGTAGAAATGGTCTTTTATCAACAGTAACCTG 2497
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2498 AAATTTGCAGAGGACCATCATGTCTGATATTAGATGCTCGATTTGGAAAGACTTT 2557
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 2558 AAACATTTAAAAAATTTTCTCTCGAATTAATAATACAGATTTTACTTGAAGAC 2617
QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2618 ACTCCAGACAGTCCGCGATATGTGGAGGGCTTGCATATGATGAGTGTAGAGAATGCTAC 2677
QY 797 AspAspProAspIleSerAlaGlyLysIleIleGlnPheCysLysThrCysAsnThrGln 816
Db 2678 GAGATCCGACATCTCAGCTGGAAATCAAGCAGTTTGTAAACCTGCAACACTCAA 2737
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2738 GTCCACCTTCATCCGAAGAGCTGAATCATATAATATAACCCAGTGTCACTTCCCAAGAC 2797
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2798 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTGGCAGAAATATGGAGTTATTGCT 2857
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2858 GTTCTCTGCATAGAAACAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGGACGATTCT 2917
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2918 GCTGCTCTTCTTTCAGCAGTATGGCGATCGGAGTGGTGTGAGATGCTCTGGAAGACTG 2977
QY 897 ProGlnValThrProCysProGluValGlyGluTyrIleLysMetSerLeuGluAspLeu 916
Db 2978 CCTCAAGTCAACCCATGCCAGAGTAGGAGTACTTGAAGATGCTCTGGAAGACTG 3037
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAlaTyr 936
Db 3038 CATTCCTTGACTCCAGGAGATCCAGGCTGTGCAGAGACTGCTTTGTGATGCATAT 3097
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrIys 949
Db 3098 ATGTGCATGTACCAGAGTCCAAATGAGTTGTACAAA 3136

RESULT 17

PCT-US02-14570-3
; Sequence 3, Application PC/TUS0214570
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; APPLICANT: Derry, Jonathan M. J.
; APPLICANT: Fanslow III, William
; APPLICANT: Dougall, William C.
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
; FILE REFERENCE: 3198-WO
; CURRENT APPLICATION NUMBER: PCT/US02/14570
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/851,673
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (392)..(3262)
; OTHER INFORMATION:

PCT-US02-14570-3

Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 1 Gaps: 5

US-09-671-687A-3 (1-949) x PCT-US02-14570-3 (1-5371)

QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 392 ATGAGTTTTCAGGCTTATGGAGCCAAAGAAAAGTCACTTCACTTCTGCGGCAATTCAGGAT 451
QY 21 PheTyrLeuLeuLeuGlnCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 452 TTTTACTTGTCTTCTCAAGAAATGCGCTTACAGACAAACAAACAAAGCTCTCTTAAA 511
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 512 GTACCGAAGGAGTATAGACAGTATATTCAAGATCGTCTGTGCGGCAATTCAGGAT 571
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 572 CTTCTCCTCAAAAGCAAGAAAATCAGATTGGATTTAAAAATTTCTAGAGCAACCTCATGCA 631
QY 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeu 99
Db 632 GTTCTCTTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTACAGAGTTTACT 691
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 692 TTGSCAAATTCACCAATTTGTGAGGAGAGGTTACGCTGTTTAAAAACAGAAAACAGACTA 751
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuAspSerGlyGluGlu 139
Db 752 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 812 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGA 871
QY 160 IlePhePheGlyValGluLeuLeuGluGluGlyGlnGlyGlnGlyPheThrAspGlyVal 179
Db 872 ATATCTTTTGGAGTTGAAATTTGCTGGAAGAGGCTGCTGCTCAAGGTTTCTACTACGG 931
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 932 TACCAAGGAAAACAGCTTTTTCAGTGTGATGAAGATTTGTGGCGTCTTTGTTCATTTG 991
QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 992 AAGCTAGAACTCATAGAAGATGATGACACTGCTTGAAGAGTATACGCAAGTCTCTGGG 1051
QY 219 AspThrMetGlnValGluLeuProLeuGluLeuAsnSerArgValSerLeuLysGly 238
Db 1052 GACAAATGCGAGTTCGAACCTTCTCTTGGAAATAAATCTCCAGAGTTTCTTTGAAGTT 1111
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 1112 GGAGAAAACAATAGAACTCTGGAACAGTTATATCTGTGATGTTTTCGCCAGGAAAAGAG 1171
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1172 TTAGGATATTTTGTGTTGTTGGATGACATGATAACCTTATTCGCAACTGGAGTGAAGAT 1231
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1232 GATGGAGTGCAGCTTTTGTAGTGTGTTGAAAGTACAATTTCTATTGCACATCAAT 1291
QY 298 AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (392) .. (3262)
US-09-851-673-3

Alignment Scores:

Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservativeness: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 33 Gaps: 5

US-09-671-687A-3 (1-949) x US-09-851-673-3 (1-5371)

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QY 1 MetSerSerGlyLeuThrSerGlnGluValThrSerProTyrTrpGluArgIle 20
DB 392 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAGTCACTTCACCCCTACTGGGAAGCGGATT 451
QY 21 PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
DB 452 TTTTACTTGCTTCTTCAAGATGCGGTTACAGACAAACAAACAAAGCTCCTTAAA 511
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
DB 512 GTACCGAAGGGAAGTATAGACAGTATATTCAAGATCGTTCTGTGGGCGATTCAAGGATT 571
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
DB 572 CCTTCTGCAAAAGCAAGAAAATCAGATTGGATTAAAAATTCATAGACAACTCATGCA 631
QY 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeu 99
DB 632 GTTCTCTTTTGTATGAAAGGATGTTGTAGAGATAAATGAAAGTTTCACAGAGTTACTT 691
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
DB 692 TTGGCAATTACCAATTGTGAGGAGGTTTCAAGCTCTTTTAAACAGAAACAGACTTAAGT 751
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
DB 752 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
DB 812 AAAATTTCTGGAGTTGTACGCTTTCAGAGGACCCCTGTTAGCAGAGGACAGCTCTCCGA 871
QY 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179
DB 872 ATATTCTTTGGAGTTGAAATTTGTGGAAGAAGTCTGTGTTCAAGTTTCACTGACGGGGTG 931
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
DB 932 TACCAAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGGTTTGTGTCATTGGAC 991
QY 199 LysLeuGlnLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
DB 992 AAGCTAGAACTCATAGAAGATGATGACACTGCACTTGGAAAGTGTATTACGCGAGTCTCTGGG 1051
QY 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
DB 1052 GACACAATGCGAGTCGAACCTTCCTCTTGGAAATAAATCAACCTCCAGAGTTCTTTGAAGGTT 1111
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
DB 1112 GGAGAAACAATAGAACTGGAACAGTTATATTCTGTGATGTTTCCACGGAAGAAAGAC 1171
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
DB 1172 TTAGGATATTTTGTGGTGTGGACATGATAACCTTATGGCAACTGGGATGGAGGATT 1231
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QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
DB 1232 GATGGAGTGCAGCTTTTGTAGTTTTCGCTGTGTGAAGTACAAATTCATTATTCACATCAAT 1291
QY 298 AspileIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314
DB 1292 GATATCATCCAGCTTTTATCAGAGAGTGTGACGAGAAAGAGGCTCTCCAACTTGCC 1351
QY 315 PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr 334
DB 1352 TTTATGTCAAGAGGTGTTGGGACAAAGTTTCATCCAGTCATAATAAACAAGGCTACA 1411
QY 335 GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly 353
DB 1412 CGATCTACCTCAGACCTCGAAATAGAAAACAGATCTGAATTTATTTATACCTTTAAATGGG 1471
QY 354 SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal 373
DB 1472 TCTTCTGTGTGACTCAAAACCACAAATCCAAATCAAAAAATACATGGTACATTAAGATT 1531
QY 374 AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPro 393
DB 1532 GCAGAGACCTTCGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCACCA 1591
QY 394 ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413
DB 1592 CCACCTCCAGCCTCTCTCTGTGAACCTCACTGACCACCGAGAACAGATTCACCTCTTTACCA 1651
QY 414 PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433
DB 1652 TTCAGTCTCACAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTG 1711
QY 434 SerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeu 453
DB 1712 TCAGCCCAAGTCTGTAATGGAAGAGCTAAACACTGCACCCGTCACAGAGAGTCCACCCTTG 1771
QY 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473
DB 1772 GCCATGCCCTCTGGGAACCTCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAG 1831
QY 474 AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal 493
DB 1832 AACCTCTCTTCTATGGGTAATCCGTTGGATCGGTTCAGGCCACCCAGGACTGAATGAAGTG 1891
QY 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513
DB 1892 CTCGCTGAGACTGGAACTGGAAGATGAGTGTGAGGCTGTACGATGGAACCTTCAGAGGC 1951
QY 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533
DB 1952 ACTCGGTATTTCACTGTGCCCTGAGAGAGGCGCTGTTTGTGAACCTGAAGAGCTGCAGG 2011
QY 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553
DB 2012 CCTGACTTAGTGTTCATCTTGCAGCCGTTTCCAATCAGATTGAGCGCTGTAACCTCT 2071
QY 554 LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573
DB 2072 TTACCATTTGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAAAATGGAA 2131
QY 574 LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer 593
DB 2132 AAGAAGCTTTGGAGATTAATATTGGGAAGAAAGAAAGGCATCCAGGCTCATTAACAATCT 2191
QY 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613
DB 2192 TGTACTTAGACTCAACCTTATCTGCTTATTGCTTTTGTAGTTCTGTTCTGGACACTGTG 2251
QY 614 LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633
DB 2252 TTACTTAGACCAAAAGAAAGAACGATGTAGAATATTATAGTGAACCAACCAAGAGCTACTG 2311
QY 634 ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653
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Db 2312 AGGACAGAAATGTTAAATCCTCAGAAATATATGATATGTTGGCCACAAAAATATG 2371
Qy 654 LysLeuArgLysLeuLeuGluLysValGluAlaLaserGlyPheThrSerGluGluLys 673
Db 2372 AAACAGGAAATACCTTGAAGAGTGGAGCTGCATCAGGATTTACCTCTGAAGAAAA 2431
Qy 674 AspProGluGluPheLeuAsnLysLeuPheHisLysLeuArgValGluProLeuLeu 693
Db 2432 GATCCTCAGGAATCTTGAATATCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTA 2491
Qy 694 LysLeuArgSerAlaGlyGlnLysValGlnAspCysTyrPheThrGlnIlePheMetGlu 713
Db 2492 AAAATAAGATCAGCAGGTCAAAAGGTACAGATTTGTTACTTCTATCAAAATTTTATGGA 2551
Qy 714 LysAsnGluLysValGlyValProThrIleGlnLeuLeuGluTyrSerPheIleAsn 733
Db 2552 AAAAATCAGAAAGTTGGCGTTCCCAACATTCAGCAGTTGTTAGAAATGGTCTTTTATCAAC 2611
Qy 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleLeuGlnMetProArgPheGly 753
Db 2612 AGTAACTGAAATTTGAGAGGACCATCATGCTGATTTATTCAGATGCCCTCGATTTGGA 2671
Qy 754 LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
Db 2672 AAAGACTTTAAACTATTTAAAAAATTTTCTCTCTGGAATTTAAATATAACAGATTTA 2731
Qy 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
Db 2732 CTTGAAGACATCCACAGACAGTGGCGATATGTGAGGGCTTGCAGATGTATGAGTGTAGA 2791
Qy 794 GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813
Db 2792 GAATGCTACGACGATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTGC 2851
Qy 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
Db 2852 AACACTCAAGTCCACCTTCATCCGAGAGGCTGAATCATANAATATAACCCAGTGTCACTT 2911
Qy 834 ProLysAspLeuProAspThrAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu 853
Db 2912 CCCAAAGACTTACCCGACTGGGACTGGAGACACGCTGCATCCCTTGCAGAAATATGAG 2971
Qy 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
Db 2972 TTATTTGCTGTTCTGTCATAGAAACCAAGCCACTATGTTGCTTTGTGAAGTATGGGAAG 3031
Qy 874 AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893
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Qy 894 PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913
Db 3092 TTCAACATTTCTCAAGTCAACCCATGCCAGAGTAGGAGAGTACTTCAAGATGTCCTG 3151
Qy 914 GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys 933
Db 3152 GAAACCTTGCATTTCTTGGACTCCAGGAGAAATCCAAAGCTGTGCACGAAGACTGCTGTT 3211
Qy 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3212 GATGCATATATGTGCATGTACAGATCCAAATGAGTTTGTATCAAA 3259

RESULT 19

US-10-755-889-489
; Sequence 489, Application US/10755889
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13

; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 489
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-489
Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 61 Gaps: 5

US-09-671-687A-3 (1-949) x US-10-755-889-489 (1-5371)

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Qy 21 PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrClnLysLeuLeuLys 40
Db 452 TTTTACTTGTCTTCTTCAAGAAATGCAGCGTTACAGACAAACAAACAAAGCTCCTTAAA 511
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 512 GTACCGAAGGAGTATAGGACAGTATATTCAGATCGTCTGTGGGCAATTCAGAGATT 571
Qy 61 ProSerAlaLysGlyLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 572 CTTCTGCAAAAGGCAAGAAAAATCAGATTGAGTTAAAAATTTCTAGAGCAACCTCATGCA 631
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 632 GTTCTCTTGTGATGAAAGGATGTTGAGAGATAAATGAAAGTTCAAGAGTTACTT 691
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 692 TTGGCAATTTACCAATTTGTGAGGAGAGGTTTCAACCTGTTTAAAAACAGAAACAGACTAAGT 751
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 752 AAAGSCCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811
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Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
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Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 1112 GGAGAAACAAATAGAAATCTGGAACAGATTATTTCTGTGATGTTTTCAGGAGAAAGAACG 1171

QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
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 QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
 Db 1232 GATGGAGTGCAGCTTTGTAGTTTGGGTGGTGTGAAGTACAAATCTATTGACACATCAAT 1291
 QY 298 AspilelePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314
 Db 1292 GATATCATCCAGCTTTTATCAGAGAGTGTGACGAGAGAAAGAGGCTCCCAAACTTGGC 1351
 QY 315 PheMetSerArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThr 334
 Db 1352 TTTATGTCAAGAGGTGTGGGGAACAAGGTTTCATCCAGTCAATAAACCAGGCTACA 1411
 QY 335 GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheThrLeuAsnGly 353
 Db 1412 GGATCTACCTCAGACCTGGAAATAGAAACAGATCTGAATATTATTTATACCTTAATGGG 1471
 QY 354 SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal 373
 Db 1472 TCTTCTGTGACTCACAAACACATCCAAATCAAAAATACATGATCAATGATGAAGTT 1531
 QY 374 AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPro 393
 Db 1532 GCAGAGAGACCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTACCA 1591
 QY 394 ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413
 Db 1592 CCACTCCAGCTCCTCTGTGAACTCACTGACCAACGAGACAGATTCACACTTTTACCA 1651
 QY 414 PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433
 Db 1652 TTCACTCTACCAAGATGCCAATACCATGGAAGTATTTGGCCACAGTCCACTTTCCTG 1711
 QY 434 SerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeu 453
 Db 1712 TCAGCCAGCTCTGTAATGGAAGAGCTAAACACTGCACCCGTCCAAGAGAGTCCACCTTG 1771
 QY 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473
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 QY 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513
 Db 1892 CTCGCTGGACTGGACTGGAGAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGC 1951
 QY 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533
 Db 1952 ACTCGGTATTTCACCTGTGCGCTGAAGAGCGCTGTTTGTGAACTGAAGAGCTGCAGG 2011
 QY 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553
 Db 2012 CCTGACTCTAGGTTTGCACTCAITTCAGCCGCTTTCCAAATCAGATTGAGCGCTGTAATCT 2071
 QY 554 LeuAlaPheGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573
 Db 2072 TTAGCATTTGGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAA 2131
 QY 574 LysGluGlyLeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSer 593
 Db 2132 AAGAAGGCTTGAGATAATGATTGGGAAGAGAGAAAGGCATCCAGGCTCAITCAATCT 2191
 QY 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613
 Db 2192 TGTTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTGTCTGTTCTGGACACTGTG 2251

QY 614 LeuLeuArgProLysGluLysGluLysValGluTyrTyrSerGluThrGlnGluLeuLeu 633
 Db 2252 TTACTTAGACCCAAAGAAAGAACGATGTAGAATATTATAGTGAAACCCCAAGAGCTACTG 2311
 QY 634 ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653
 Db 2312 AGGACAGAAATTTGTAATCTCTGAGATATATGATATGTGTGCCACAAAAATATG 2371
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 Db 2372 AAATGAGGAAATACTTTGAAAGGTGGAGGCTGCATCAGGATTTTACCTCTGAAGAAAA 2431
 QY 674 AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693
 Db 2432 GATCCTGAGGAATTTCTGAATATTCTGTTTTCATATATTTAAGGGTAGAACCTTTGCTA 2491
 QY 694 LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713
 Db 2492 AAATAAGATCAGCAGGTCAAAGGTACAAGATTGTACTTCTATCAAAATTTTATGGAA 2551
 QY 714 LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsn 733
 Db 2552 AAAAATGAGAAAGTTGGGCTTCCACAAATTCAGAGTTGTTAGATGGTCTTTTATCAAC 2611
 QY 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753
 Db 2612 AGTAACCTGAAATTTGCAGAGCACCATCATGCTCTGATTATTTTATCAGATGCTCGATTGGA 2671
 QY 754 LysAspPheLysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
 Db 2672 AAAGACTTTAAACTATTTTAAAAAAATTTTCTCTCTGGAATTTAAATATAACAGATTTA 2731
 QY 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
 Db 2732 CTTGAGACACTCCAGACAGTCCGATATGTGGAGGCTTGCATATGATGAGGTAGA 2791
 QY 794 GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813
 Db 2792 GAATGCTACGACGATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAACTGC 2851
 QY 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
 Db 2852 AACACTCAAGTCCACTTTCATCCGAAAGAGGTGAATCATATAATAAACCCAGTGTCACTT 2911
 QY 834 ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu 853
 Db 2912 CCCAAAGACTTACCAGACTGGGACTGGAGACACGGCTGCATCCCTGCCAGAAATATGGAG 2971
 QY 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
 Db 2972 TTATTTGCTGTTCTTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAG 3031
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 Db 3092 TTCAACATTCCTCAAGTCAACCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTG 3151
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 Db 3152 GAAGCTTGCATTCCTTGGACTCCAGGAGAAATCAAAGCTGTGACGAGACTGTCTTGT 3211
 QY 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
 Db 3212 GATCATATATGTGATGTACAGAGTCCACAAATGAGTTGTACAAA 3259

RESULT 20

US-10-760-678-3

; Sequence 3, Application US/10760678

; GENERAL INFORMATION:

; APPLICANT: Derry, Jonathan

; APPLICANT: Fanslow, William
; APPLICANT: Dougall, William
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
; FILE REFERENCE: 3198
; CURRENT APPLICATION NUMBER: US/10/760,678
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US/09/851,673
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (392)..(3262)
US-10-760-678-3

Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 61 Gaps: 5

US-09-671-687a-3 (1-949) x US-10-760-678-3 (1-5371)

Qy 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgile 20
Db 392 ATGAGTTTCAGGCTTATGAGGCAAGAAAAGTCACTTCCACCTACTGGGAAGCGGATT 451
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 452 TTTTACTTGTCTTCAAGAAATGACAGCTTACAGACAAAACAAACAGAAAGCTCTTAAA 511
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgile 60
Db 512 GTACCGAAGGGAAGATAGGACAGTATATTCAGATGCTTCTGTGGGCAATTCAGGATT 571
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 572 CCTTCTGCNAAAGGCAAGAAAATCAGATTGGATTAAAAATTCAGACCACTCATGCA 631
Qy 81 ValLeuPheValAspGlu---AspValValGluLysAsnGlnLysPheThrGluLeu 99
Db 632 GTTCTCTTTGTGATGAAAAGCATGTTGTAGAGATAAATGAAAAGTTTACAGAGTTACT 691
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 692 TTGGCAATTAACAAATGTAGAGAGAGGTTCAGCTGTTTAAAAACAGAAAACAGACTAAGT 751
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 752 AAGGCTTCCNAAATAGAGTGGGCTGCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 812 AAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGGACAGTCTCCGGA 871
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 872 ATATTCTTTGGAGTTGAATTTCTCGAAGAAAGTCTGCTCAAGGTTTTCACCTGACGGGGTG 931
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 932 TACCAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGGTGTTGTTCATTTGGAC 991
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 992 AAGCTAGAACTCATAGAAGATGATGACACTGCATTTGGAAAGTATTACGACAGGTCCTGGG 1051

Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 1052 GACACAATGCAGGTCGAACCTTCTCTTTGGAAATAACTCCAGAGTTTCTTTGAAGTT 1111
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 1112 GGAGAAACAATAGAATCTGGAACAGTTATTTCTGTGATGTTTTCGACGAAAAGAAC 1171
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1172 TTAGGATATTTTGTGGTGTGACATGATACCTTATTGGCAACTGGGATGGAAGATT 1231
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1232 GATGGAGTGCAGCTTTGTAGTTTTCGGTGTGTTGAAAGTACAAATCTATTGCACATCAAT 1291
Qy 298 AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314
Db 1292 GATATCATCCAGCTTTTATCAGAGAGTGTGACGACGAAAGGAGGCTCCCAAACTTGCC 1351
Qy 315 PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr 334
Db 1352 TTTATGTCAGAGGTTTGGGGACAAAGGTTTCATCCAGTCATAATAAAACCAAGGCTACA 1411
Qy 335 GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly 353
Db 1412 GATCTACTCAGACCTTGGAAATAGAAACAGATCTGAATTTATTTATACCTTTAAATGGG 1471
Qy 354 SerSerValAspSerSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal 373
Db 1472 TCTTCTGTGACTCACACCAACCAATCCAAATCAAAAATATACATGTTGATGATGAAGTT 1531
Qy 374 AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerPro 393
Db 1532 GCAGAAGACCTTGCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCA 1591
Qy 394 ProLeuGlnProProValAsnSerLeuThrGluAsnArgPheHisSerLeuPro 413
Db 1592 CCATCCAGCTCTCTCTGTGAACCTCACTGACCCAGGAGAACAGATTCCACTCTTTACCA 1651
Qy 414 PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433
Db 1652 TTCAGTCTCACCAAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTG 1711
Qy 434 SerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProLeu 453
Db 1712 TCAGCCCACTGTAAATGGAAGAGCTAAACACTGCACCCGCTCCAAAGAGAGTCCACCTTG 1771
Qy 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473
Db 1772 GCCATGCTCTCTGGGAACCTCACATGGTCTAGAAGTGGGCTCAATTGGCTGAAGTAAAGAG 1831
Qy 474 AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal 493
Db 1832 AACCTCTCTTCTATGGGTAAATCGTTGGATCGGTGAGCCACAGGACTGAATGAAGTG 1891
Qy 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513
Db 1892 CTCGCTGGACTGGAACCTGGAAGATGAGTGTGCAGGCTGTACGGATGGAACCTTCAGAGGC 1951
Qy 514 ThrArgTyrPheThrCysAlaLeuLysIleAlaLeuPheValLysLeuLysSerCysArg 533
Db 1952 ACTCGGTATTTTCACTGTGCCCTTGAAGAAAGCGCTGTTGTGTAAGCTGAAGAGCTGCAGG 2011
Qy 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553
Db 2012 CCTGACTCTAGTTTGCATCATTTGCGCCGGTTTCCAATCAGATTGAGCGCTGTAACTCT 2071
Qy 554 LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573
Db 2072 TTAGCATTTGGAGGCTACTTAAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAA 2131
Qy 574 LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer 593


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Db 2132 AAGAAGGCTTGGAGATAAATGATTTGGGAAGAAAGGCATCCAGGGTCATTACAATTCT 2191
QY CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613
Db 2192 TGTACTTAGACTCAACCTTATCTGCTTATTTAGTCTGTTCTGGACACTGTG 2251
QY LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeu 633
Db 2252 TTACTTAGACCCAAAGAAAGAACGATGTAGATATTATAGTGAACCCAGAGCTACTG 2311
QY ArgThrGluLeuValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653
Db 2312 AGACAGAAATGTTAATCTCTGAGAAATATGATATGATGTGTGCACAAAATATG 2371
QY LysLeuArgLysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLys 673
Db 2372 AACTGAGGAATATCTTGAAGGTGAGGCTGCATCAGGATTACTCTGGAAGAAA 2431
QY AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693
Db 2432 GATCCTGAGGAATCTTGAATATCTGTTTCATCATATTTAAGGGTAGAACCTTTGCTA 2491
QY LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713
Db 2492 AAAATAAGATCAGCAGGTCAAAAGGTAACAAGTTGTACTCTATCAAAATTTTATGGAA 2551
QY LysAsnGluLysValGlyValProThrIleGlnLeuLeuGluTyrSerPheIleAsn 733
Db 2552 AAAATGAGAAAGTTGCGTGTCCACAAATTCAGCAGTTGTAGAAATGGTCTTTATCAAC 2611
QY SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753
Db 2612 AGTAACCTGAAATTCAGAGGACCAATCATGTCGATTATTCAGATCGCTCGATTTGGA 2671
QY LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
Db 2672 AAAGACTTTAAACTAATTAATAAAAAATTTTCTCTCTGGAATTAATAACAGATTTA 2731
QY LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
Db 2732 CTTGAAGACACTCCCAGACAGTCCGGATATGTGGAGGGCTTGCATGTATGATGTAGA 2791
QY GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813
Db 2792 GAATGCTACGACGATCCGGACATCTCAGCTGGAAAATCAAGCAGTTTGTGTAACCTGC 2851
QY AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
Db 2852 AACACTCAAGTCCACCTTCATCCGAAGAGGCTGAATCATATAATATAACCCAGTGCATT 2911
QY ProLysAspLeuProAspThrAspThrArgHisGlyCysIleProCysGlnAsnMetGlu 853
Db 2912 CCCAAAGACTTACCCGACTCGGACTGGAGACAGGCTGCATCCCTTGCCAGAAATATGGAG 2971
QY LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
Db 2972 TTATTTGCTGTTCTCTGCTAGAAAACAGCCATATGTTCTTTTGTGAAGTATGGGAG 3031
QY AspAspSerAlaThrLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893
Db 3032 GACCATTCCTGCTGCTCTCTTTTGACAGCATGCGCGATCGGATGGTGTGAGATGGC 3091
QY PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913
Db 3092 TTCACATTCCTCAAGTCAACCCATGCCCCAAGAGTAGGAGACTTTGAAGATGTCTCTG 3151
QY GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys 933
Db 3152 GAAGACCTGCTATTCCTTGACTCCAGAGAAATCAAGGCTGTGCACCAAGACTGCTTTGT 3211
QY AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
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Db 3212 GATGCATATATGTGCATGTACAGAGTCCAAACAATGAGTTTGTACAAA 3259
RESULT 21
US-10-887-553A-199
; Sequence 199 Application US/10887553A
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-199

Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: Gaps: 5

US-09-671-687A-3 (1-949) x US-10-887-553A-199 (1-5371)

QY 1 MetSerSerGlyLeuTyrSerGlnGluLysValThrSerProTyrTyrGluGluArgIle 20
Db 392 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAGTCACTTCACCCTACTTGGAGAGCGGATT 451
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 452 TTTTACTTGTCTTCTCAAGAATGCAGCTTACAGCAACAAACAAAGTCTCTTAAA 511
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 512 GTACCGAAGGGAAGTATAGGACAGATATATTCAAGATCGTCTCTGTGGGCAITTCAGGATT 571
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 572 CCTTCTCAAAAGCAAGAAAATCAGATTGCATTAAAAATTTCTAGAGCAACCTCATGCA 631
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 632 GTTCTCTTGTGTGAAGAAAGGATGTTGTAGAGATAAATGAAGTTTACAGAGTTTACTTT 691
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 692 TTGGCAATTAACCAATTTGTAGAGAGAGGTTTACGCTGTTTAAAAACAGAAACAGACTAAGT 751
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 752 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 812 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGA 871
QY 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 872 ATATTTCTTGGAGTTGAATTCCTGGAAGAAAGTCTGTGTCAAGGTTTCACTGACGGGGTG 931
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 932 TACCAGGGAACACAGCTTTTTCAGTGTGATGAAGATTTGTGGCGTCTTTGTTCATTGGAC 991
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Qy	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218		Db	2072	TTAGCATTTGGAGGCTACTTAAGTGAAGTAAAGAAATACTCCACCAAAATGGAA	2131	
Db	992	AAGCTAGAACTCATAGAAGATGATGACATGCAATGGAAAGTATTACGACAGGTCCTGGG	1051		Qy	574	LysGluGlyLeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSer	593	
Qy	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238		Db	2132	AAAGAAGGCTTGGAGATTAATGATGGGAAGAAAGACATCCAGGGTCATTACAAATCT	2191	
Db	1052	GACAAATGAGGTCGAACCTCCCTTTGGAAATAAATCCAGAGTTTCTTTGAAGGTT	1111		Qy	594	CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal	613	
Qy	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258		Db	2192	TGTTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTG	2251	
Db	1112	GGAAACAATAGAAATCTGGACAGTATATCTGTGATGTTTGGCCAGGAAGAAGAC	1171		Qy	614	LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu	633	
Qy	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe	278		Db	2252	TTACTTAGACCCCAAGAAAGAACGATCTAGAAATATTATAGTGAACCAACGAGCTACTG	2311	
Db	1172	TTAGGATATTTTGTGTGTGGACATGGATAACCTATTGGCAACTGGGATGGAGATTT	1231		Qy	634	ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet	653	
Qy	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297		Db	2312	AGGACAGAAATTTGTAATCTCTGAGAAATATATGGATATGTGTGCCACAAAAATATG	2371	
Db	1232	GATGGAGTGCAGCTTGTAGTTTTTGGCGTGTGTGAAAGTACAATTTCTATTTCACATCAAT	1291		Qy	654	LysLeuArgLysIleLeuGluLysValGluAlaAspSerGlyPheThrSerGluGluLys	673	
Qy	298	AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla	314		Db	2372	AAACTGAGAAATACTTTGAAAGAGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAA	2431	
Db	1292	GATATCATCCAGCTTATATCAGAGAGTGTGACGAGGAAGAGGCGCTCCCAAACTTGCC	1351		Qy	674	AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu	693	
Qy	315	PheMetSerArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThr	334		Db	2432	GATCCTGAGGAATCTTGAATATTTCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTA	2491	
Db	1352	TTTATGTCAAGAGTGTGGGACAAAGTTTCATCCAGTCAATATAAACCAAGGCTACA	1411		Qy	694	LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu	713	
Qy	335	GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly	353		Db	2492	AAAATAAGATCAGCAGGTCAAAAGGTACAAAGTGTACTTCTATCAAAATTTTATGGAA	2551	
Db	1412	GGATCTACCTCAGACCCCTGGAAATAGAAACAGATCTGAATTTATTTATACCTTAATGGG	1471		Qy	714	LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsn	733	
Qy	354	SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal	373		Db	2552	AAAATGAGAAAGTTGGCGTTCCCAATTCAGCAGTTGTTAGAAATGGTCTTTTATCAAC	2611	
Db	1472	TCCTCTGTGACTCACAAACCAATCCAAATCAAAATAATCATGGTACATTTGATGAAGTT	1531		Qy	734	SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly	753	
Qy	374	AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerPro	393		Db	2612	AGTAACCTGAAATTTGCAGAGCCACCATCATGCTCTGATTAATTCAGATGCTCGATTGGA	2671	
Db	1532	GCAGAAACCTCGAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTCACCA	1591		Qy	754	LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu	773	
Qy	394	ProLeuGlnProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro	413		Db	2672	AAAGACTTTAAACTATTATAAAAAATTTTCTCTCTGGAATTAATAATAACAGATTTA	2731	
Db	1592	CCATCCAGGCTCTCTCTGTGAACCTCACTGACCCAGAGAACAGATCCACTCTTTACCA	1651		Qy	774	LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg	793	
Qy	414	PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu	433		Db	2732	CTTGAAGACACTCCAGACAGTCCGGATATGTGGAGGCTTGGCAATGTATCAGTGTAGA	2791	
Db	1652	TTGAGTCTCACAAGATGCCAATACCAATGGAAGTATTTGGCCACAGTCCACTTTCTCTG	1711		Qy	794	GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys	813	
Qy	434	SerAlaGlnSerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeu	453		Db	2792	GAATGCTACGACGATCCGGACATCTCAGCTGGAAAAATCAACGAGTTTTTGTAAAAACCTGC	2851	
Db	1712	TCAGCCCGAGTCTGTAATGGAAAGAGCTAAACACTGCACCCGCTCCAGAGAGTCCACCTTG	1771		Qy	814	AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu	833	
Qy	454	AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu	473		Db	2852	AACACTCAAGTCCACTTTCATCCGAAAGAGGCTGAATCATATAATAACCCAGTGCACCT	2911	
Db	1772	GCCATGCTCTCTGGAACTCATAGTGTCTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGAG	1831		Qy	834	ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu	853	
Qy	474	AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal	493		Db	2912	CCCAAGACTTACCAGACTGGGACTGGAGACACGCTGCATCCCTTGCAGAAATATGGAG	2971	
Db	1832	AAACCTCTTCTATGGGTAAATCCGTTGGATCGGTACGCCACAGGACTGAAATGAAGTG	1891		Qy	854	LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys	873	
Qy	494	LeuAlaGlyLeuLeuLeuAspGluCysAlaGlyCysThrAspGlyThrPheArgGly	513		Db	2972	TTATTTGCTGTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAG	3031	
Db	1892	CTCGCTGGACTGGAACTGGAAAGATGAGTGTGACGGCTGTACGGATGGAACTTCAGAGGC	1951		Qy	874	AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly	893	
Qy	514	ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg	533		Db	3032	GACGATTTCTGCTGCTCTTCTTTGACAGCATGGCCGATCGGGATGGTGGTTCAGAAATGCG	3091	
Db	1952	ACTCGGTATTCACCTGTGCTGCTGAGAGAGCGCTGTTTGTGAACCTGAAGAGCTGCAGG	2011		Qy	894	PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu	913	
Qy	534	ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer	553		Db	3092	TTCAACATTTCTCAAGTCAACCCATGCCAGAAAGTAGGAGAGTACTTGAAGATGCTCTCTG	3151	
Db	2012	CCTGACTCTAGGTTTGCATCTTTCAGCGCGTTTCCAATCAGATTTGAGCGCTGTAACCTCT	2071		Qy	914	GluAspLeuHisSerLeuAspSerArgIleGlnGlyCysAlaArgLeuLeuCys	933	
Qy	554	LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu	573						

Db 3152 GAAGACCTGCATTCCTTGGACTCCAGAGAAATCAAGGCTGTGCACGAAGACTCCTTTGT 3211
Qy 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3212 GATGCATATATGTGCATGTACCGAGAGTCCAACAATGAGTTGTACAAA 3259

RESULT 22

US-60-440-068-489
; Sequence 489, Application US/60440068
; GENERAL INFORMATION:
; APPLICANT: NADLER, STEVEN G.
; APPLICANT: CARMAN, JULIE
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
; TITLE OF INVENTION: NF-KB PATHWAY
; FILE REFERENCE: 3053-4191
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 489
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-440-068-489

Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 79 Gaps: 5

US-09-671-687a-3 (1-949) x US-60-440-068-489 (1-5371)

Qy 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 392 ATGAGTTTCAGGCTTATGAGCCCAAGAAAGTCACTCCCTACTTGGGAAGCGGATT 451
Qy 21 PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 452 TTTTACTTCTCTTCAAGAATGCAGCTTACAGACAAACAAACACAAAGCTCTTAA 511
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 512 GTACCGAAGGAGATATAGACAGTATATTCAGATCGTTCTGTGGGCAATTCAGGATT 571
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
Db 572 CCTTCTGCAAAAGGCAAGAAATAATCAGATTGGATTAAATAATTCAGACCACTCATGCA 631
Qy 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGlnLysPheThrGluLeuLeu 99
Db 632 GTTCTCTTTGTTGATGAAAGGATGTGTAGAGATAAATGAAAGTTTCAAGAGTTACTT 691
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgenArgLeuSer 119
Db 692 TTGGCAATTACCATTGTGAGGAGAGGTCAGGCTGTTTAAACAGAAACAGACACTAAGT 751
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 752 AAAGGCTCCAAATAGACGCTGGGCTGCTCTGTGAAGTAGTACAGTGTGAGTCTGGGGAGAA 811
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 812 AAATTTCTCGGAGTTTACGCTTCAGAGGACCCCTGTAGCAGAGGACAGTCTCCGGA 871
Qy 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179
Db 872 ATATTCTTGGAGTTGAATTCGTGGGAAGAGGTGCTGGTCAAGGTTTCACTGACGGGGT 931
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198

Db 932 TACCAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTCTTGTTCATTTGGAC 991
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 992 AAGCTAGAACTCATAGAAGATGATGACACTGCAATTTGGAAGTGATTAACGAGGTCCTGG 1051
Qy 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 1052 GACACAATGCAGGTCGAACCTTCTCTTTTGGAAATAAACTCCAGAGTTCTTTTGAAGGTT 1111
Qy 239 GlyGlnThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 1112 GGAGAAACAAATAGAAATCTGSAACAGTTATATCTGTGATGTGTTTCCAGAAAGAAAGC 1171
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTyrAspGlyArgPhe 278
Db 1172 TTAGGATATTTTGTGTGTGGACATGATTAACCTTATTTGGCACTGGGATGGAGATT 1231
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1232 GATGAGTGCAGCTTTGTAGTTTTCGCTGTGTGAAAGTACAATTTCTATTGCACATCAAT 1291
Qy 298 AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314
Db 1292 GATATCATCCAGCTTTATTCAGAGAGTGTGACGAGAAAGAGGCGCTCCCAAACTTGC 1351
Qy 315 PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr 334
Db 1352 TTTATGTCAGAGGTTTGGGACAAAGGTTTCATCCAGTCATAATAAACCAAGGCTACA 1411
Qy 335 GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly 353
Db 1412 GGATCTACCTCAGACCCCTGGAAATAGAAACAGATCTGAATTTATTTATACCTTAAATGG 1471
Qy 354 SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTyrTyrIleAspGluVal 373
Db 1472 TCTTCTGTGACTCACAACCAATCCAAATCAAAATACATAATGATGATGATGATGATGAT 1531
Qy 374 AlaGluAspProAlaLysSerLeuThrGluLeuSerThrAspPheAspArgSerPro 393
Db 1532 GCAGAAACCCCTGCANAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTCTTCCACA 1591
Qy 394 ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413
Db 1592 CCCTCCAGGCTCTCTCTGTGAACTCACTGACCAACGAGAACAGATTCACCTCTTTTACCA 1651
Qy 414 PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433
Db 1652 TTCAGTCTCACCAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGT 1711
Qy 434 SerAlaGlnSerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeu 453
Db 1712 TCAGCCAGCTGTGTAATGGAAGAGCTAAACACTGCACCCGCTCCAAGAGAGTCCACCTTG 1771
Qy 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473
Db 1772 GCCATGCTCTGGAACTCACATGGTGTAGAGTGGGCTCATTTGGCTGAAAGTTAAGAG 1831
Qy 474 AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal 493
Db 1832 AACCTCTCTTCTATGGGTAATCCGTTGGATCGTGCAGCCACCAAGGACTGAATGAAGTG 1891
Qy 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513
Db 1892 CTCGCTGCAGTGGAACTGGAAGATGAGTGTGCAGGCTGTACGGATGGAACCTTCAAGAGC 1951
Qy 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533
Db 1952 ACTCGGTATTTTCACTGTGCCCTGGAAGGCGCTGTTTGTGAAACTGAAGAGCTGCAGG 2011
Qy 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553
Db 2012 CCTGACTCTAGGTTTGATCATTCACGCGGTTTCCAAATCAGATTGAGCGCTGTAACTCT 2071

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Qy 554 LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573
Db 2072 TTAGCACTTTGGAGGCTACTTAAAGTGAAGTAGTAGAAGAAAAATCTCCACCAAAAAATGGAA 2131
Qy 574 LysGluGlyLeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSer 593
Db 2132 AAAGAAGGCTTGGAGATAATGATTTGGGAAGAAAGGCATCCAGGCTCATTAACAAATCTCT 2191
Qy 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613
Db 2192 TGTACTTAGACTCAACCTTATTCTGCTTATTGCTTTTATTGCTTTTATTGCTTTGACACACTGTG 2251
Qy 614 LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633
Db 2252 TTACTTAGACCCAAAGAAAGAACGATGTAGATAATTATAGTGAACCCCAAGAGCTACTGT 2311
Qy 634 ArgThrGluIleValLeuProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653
Db 2312 AGACAGAAATTTTAACTCTCGAGAAATATATGGATATGTGTGTGCCACAAAAATTTATG 2371
Qy 654 LysLeuArgLysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLys 673
Db 2372 AAACCTGAGGAAATACTTTGAAAGGTGGAGCTGCATCAGATTTACTCTGGAAGAAAA 2431
Qy 674 AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693
Db 2432 GATCCTGAGGAATCTTGAATATTCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTA 2491
Qy 694 LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713
Db 2492 AAAATAAGATCAGCAGGTCAAAAGGTCAAAAGTTGTTACTTCTATCAAAATTTTATGGAA 2551
Qy 714 LysAsnGluLysValGlyValProThrIleGlnLeuLeuGluTyrSerPheIleAsn 733
Db 2552 AAAAATGAGAAAGTTGGCGTTCCACAAATTCAGCAGTTGTAGAAATGGTCTTTTATCAAC 2611
Qy 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753
Db 2612 AGTAACTGAAATTTGCAGAGGACCACTCATGCTGATTAATCAGATGCCCTCGATTTGGA 2671
Qy 754 LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
Db 2672 AAAGACTTTTAAACTATTATAAAAAATTTTCTCTCGAAATTTAAATATAACACAGATTTA 2731
Qy 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
Db 2732 CTTGAAGACACTCCCGACACTGCGGATATGTGGAGGGCTTGCAATGTATGAGTGATGA 2791
Qy 794 GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813
Db 2792 GAATGCTACGACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTCGC 2851
Qy 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
Db 2852 AACACTCAAGTCCACCTTTCATCCGAAGAGGCTGATCATATAATATAACCCAGTGTCACTT 2911
Qy 834 ProLysAspLeuProAspThrPaspThrArgHisGlyCysIleProCysGlnAsnMetGlu 853
Db 2912 CCCAAAGACTTACCGACTGGGACTGGAGACACGGCTGCATCCCTTCCAGAAATATGGAG 2971
Qy 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
Db 2972 TTATTTGCTCTTCTGTCATAGAAACAAAGCCACTATGTGCTTTTGTGAAGATATGGGAAG 3031
Qy 874 AspAspSerAlaThrLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893
Db 3032 GACGATTCGCTGGCTCTTCTTTTGACAGCATGGCCGATCGGGATGTGTGTCAGAAATGGC 3091
Qy 894 PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913
Db 3092 TTCAACACTTCTCAAGTCACCCCATGCCAGAGTAGGAGTACTTTGAAGATGTCCTCTG 3151
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Qy 914 GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys 933
Db 3152 GAAGACCTGCATTCCTTGGACTCCAGGAGATCCAAAGCTGTGCAGAGACTGCTTTGT 3211
Qy 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3212 GATCATATATGTGCATGTACCCAGAGTCCAAACAATGAGTTGTGTACAAA 3259
RESULT 23
US-60-469-757-489
; Sequence 489, Application US/60469757
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 PSpI
; CURRENT APPLICATION NUMBER: US/60/469,757
; CURRENT FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 489
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-469-757-489
Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 80 Gaps: 5
US-09-671-687A-3 (1-949) x US-60-469-757-489 (1-5371)
Qy 1 MetSerSerGlyLeuTyrSerGlnGluLysValThrSerProTyrTrpGluArgIle 20
Db 392 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAGTCATCTTCACTCTCTGGGAAGCGGATT 451
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 452 TTTTACTTGTCTTCAAGAAATGCGGTTACAGACAAACAAACACAAAGCTCCTTAA 511
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 512 GTACCGAAGGGAAGTATAGGACAGTATATTCAGATCCTTCTGTGGGCAATTCAGAGATT 571
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 572 CCTTCTGCNAAGGCAAGAAAATCAGATTGGATTAAAAATTTAGAGCAACTCATGCA 631
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 632 GTTCTCTTTTGTGATGAAAGGATGTTGTAGAGATAAATGAAAGTTTACAGAGTTACTT 691
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 692 TTGCAATTTACCAATTTGTAGAGAGAGGTTTCAGCCTGTTTAAAAACAGAAACAGACTAAGT 751
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 752 AAGGCTTCCAAATAGAGCTGGGCTGCTCTGTGAAGTACAGTGAATCTGGGAGAGAA 811
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 812 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTTAGCAGAGAGGACACTCCGGA 871
Qy 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179
Db 872 ATATTTCTTGGAGTTGAATTTCTCGAAGAGGTCGTGTCTCAAGGTTTCACTGACGGGGTG 931
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
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Db	932	TACCAAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTCATTGGAC	991
Qy	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218
Db	992	AAGCTAGAACTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACGCAGGTCTCTGGG	1051
Qy	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238
Db	1052	GACACAAATGCGAGTGGAACTTCTCTCTTGGAAATAAACTCCAGAGTTCTCTTGAAGTT	1111
Qy	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258
Db	1112	GGAGAAACAATAGAACTCGAAACAGTTATATCTGTGATGTGTTCGCCAGGAAAGAAGC	1171
Qy	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAenTrpAspGlyArgPhe	278
Db	1172	TTAGGATAATTTGTTGGTGGACATGGATAACCTATTGGCAACTGGGATGGAGATTT	1231
Qy	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297
Db	1232	GATGGAGTGCAGCTTTGTAGTTTTCGTGTGTTGAAAGTACAATTTCTATTGCACATCAAT	1291
Qy	298	AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla	314
Db	1292	GATATCATCCAGCTTTATCAGAGAGTGTGCGCAGGAAAGGAGGCCCTCCCAACTTGGC	1351
Qy	315	PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr	334
Db	1352	TTTATGTCAAGAGGTGTGGGCAAAAGGTTCTCCAGTCAATAAACCAGGCTGACA	1411
Qy	335	GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly	353
Db	1412	GGATCTACCTCAGACCCCTGGAATAGAAACAGATCTGAATTTATATACCTTAATGGG	1471
Qy	354	SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal	373
Db	1472	TCTTCTGTTGACTCACAAACACAAATCCAAATCAAAATAACATGTTACATTGTAAGTT	1531
Qy	374	AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPro	393
Db	1532	GCAGAGACCCCTGAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCACCA	1591
Qy	394	ProLeuGlnProProProValAsnSerLeuThrThruAsnArgPheHisSerLeuPro	413
Db	1592	CCACTCCAGCTCTCTCTGTAACCTACTGACCAACCGAGACAGATTCCACTCTTTACCA	1651
Qy	414	PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu	433
Db	1652	TTCAGTCTCACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTG	1711
Qy	434	SerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeu	453
Db	1712	TCAGCCCGAGTCTGTAATGGAAGAGCTAAACACTGCACCCGCTCCAAGAGAGTCCACCCCTG	1771
Qy	454	AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu	473
Db	1772	GCCATGCCCTCCGGAACTCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAG	1831
Qy	474	AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal	493
Db	1832	AACCTCTCTTATGGGGTAAATCCGTTGGATCGGTGAGCCACGAGACTGAATGAAGTG	1891
Qy	494	LeuAlaGlyLeuGluLeuAspGluCysAlaGlyCysThrAspGlyThrPheArgGly	513
Db	1892	CTCGCTGGACTGGAATGGAAGATGAGTGTGCAAGCTGTACGGATGGAACCTTCAGAGGC	1951
Qy	514	ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg	533
Db	1952	ACTCGGTATTTCACTTCCCTGCGCTGGAAGAGCGGCTGTTGTGAAACTGGAAGAGCTGCAGG	2011
Qy	534	ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer	553
Db	2012	CCTGACTTAGGTTTGATCATCTTGACAGCCGGTTTCCAAATCAGATTGAGCGCTGTAACCTCT	2071
Qy	554	LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu	573
Db	2072	TTAGCAITTTGGAGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAA	2131
Qy	574	LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer	593
Db	2132	AAAGAAGCTTTGGAGATAATGATTGGGAAGAAAGGATCCAGGGTCATTACAAATCTCT	2191
Qy	594	CystTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal	613
Db	2192	TGTTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTG	2251
Qy	614	LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu	633
Db	2252	TTACTTAGACCCAAAGAAAGAACGATGATAGATATATATAGTGAACCCAGAGCTACTG	2311
Qy	634	ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet	653
Db	2312	AGGACAGAAATGTTAATCTCTGAGAATATATGGATATGTGTGTCACCAAAATATTG	2371
Qy	654	LysLeuArgLysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLys	673
Db	2372	AACTGAGGAAATACTTGAAGGTGGAGCTGCATCAGGATTTTACCTCTGAAGAAAA	2431
Qy	674	AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu	693
Db	2432	GATCTCAGGAATTTCTTGAATATTTCTGTTTCATCATATTTTAAGGGTAGAACCTTGTCTA	2491
Qy	694	LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu	713
Db	2492	AAATAAGATCAGCAGGTCAAAAGGTACAGATTGTTACTTCTATCAAAATTTTATGGAA	2551
Qy	714	LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsn	733
Db	2552	AAAAATGAGAAAGTTGGCGTTCCACAAATTCAGCAGTTGTTAGAAATGCTTTTATCAAC	2611
Qy	734	SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly	753
Db	2612	AGTAACCTGAAATTTGAGAGGCCACCATCATGTCTGATTATTACAGATCCCTCGATTGGA	2671
Qy	754	LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu	773
Db	2672	AAAGACTTTAAACTATTTTAAAAAAATTTTCTCTCTGGAAATTAATAATACAGATTTA	2731
Qy	774	LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg	793
Db	2732	CTTGAAGACACTCCACAGACAGTCCGGATATGTGGAGGGCTTGCAATGTATGAGTGTAGA	2791
Qy	794	GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys	813
Db	2792	GAATGCTACGACGATCCGGACATCTCAGCTGGAATAATCAAGCAGTTTTTGTAAAAACCTGC	2851
Qy	814	AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu	833
Db	2852	AACACTCAAGTCCACCTTCATCCGAAGAGGCTGAATCATATAATATAAATCCAGTGTACATT	2911
Qy	834	ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu	853
Db	2912	CCCAAGACTTACCCGACTGGGACTGGAGACACCGCTGCATCCCTTGGCAGAAATATGGAG	2971
Qy	854	LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys	873
Db	2972	TTATTTGCTGTTCTCGATAGAAACAAAGCCACTATGTGCTTTTGTGAAGTATGGGAAG	3031
Qy	874	AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly	893
Db	3032	GACGATTTCCCTCGGCTCTTCTTTTGACAGCATGCCCATCGGGATGGGTGAGAAATGCG	3091
Qy	894	PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu	913
Db	3092	TTCAACATTTCTCAAGTCAACCCATGCCCCAGAGTAGGAGAGTACTTGAAGATGTCTCTG	3151

Qy	914	GlutAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys	933
Db	3152	GAAAGACCTGCAATTCCTTGGACTCAGAGAGATCCAAAGCTGTGCACGAAGACTGCTTTGT	3211
Qy	934	AspAlaTyMetCysMetTyGlnSerProThrMetSerLeuTyLys	949
Db	3212	GATGCATATGTGCACTGTAACAGAGTCCAAACATGAGTTGTGTACAAA	3259

RESULT 24

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US-60-710-726-1537
; Sequence 1537, Application US/60710726
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Serre, Valerie
; APPLICANT: Eerdewegh, Paul V
; APPLICANT: Little, Randall D
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: GeneMap of the human genes associated with Crohn's disease
; FILE REFERENCE: 059908-5009-PR
; CURRENT APPLICATION NUMBER: US/60/710, 726
; CURRENT FILING DATE: 2005-08-24
; NUMBER OF SEQ ID NOS: 20166
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1537
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homosapiens
US-60-710-726-1537

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Alignment Scores:			
Pred. No.:	0	Length:	5371
Score:	4971.50	Matches:	948
Percent Similarity:	99.16%	Conservative:	0
Best Local Similarity:	99.16%	Mismatches:	1
Query Match:	98.76%	Indels:	7
DB:	83	Gaps:	5

US-09-671-687A-3 (1-949) x US-60-710-726-1537 (1-5371)

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Db	392	ATGAGTTTCAGGCTTATGAGCCACAGAAAAGTCACTTCACCCCTACTGGGAAGAGGGGATT	451
Qy	21	PheTyrLeuLeuGlnGlnCysSerValThrAspLysGlnThrClnLysLeuLeuLys	40
Db	452	TTTTACTTGCCTCTTCACAGAAATGCAGCGTTACAGACAAACAAACAAAGCTCCTTAAA	511
Qy	41	ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle	60
Db	512	GTACCGAAGGGGAAGTATAGGACAGATATATCAAGATCGTTCTGTGGGGGATTCACAGGATT	571
Qy	61	ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAla	80
Db	572	CCTTCTGCAAAAGGCAAGAAAATCAGATTGGATTAAAAATTTCTAGAGCAACCTCATGCA	631
Qy	81	ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGlnLeuLeu	99
Db	632	GTTCTCTTTGTGATGATAAAGGATGTTGTAGAGATAAATGAAAGTTACACAGATTACTT	691
Qy	100	LeuAlaIleThrAsnCysGlnClnuArgPheSerLeuPheLysAsnArgAsnArgLeuSer	119
Db	692	TTGGCAATTACCAATTGTGAGAGAGGTTTCACCTGTTTTTAAAAACACAGAACTAAGT	751
Qy	120	LvsGlvLeuGlnIleAspValGlvCvsProValLysValGlnLeuArgSerGlvGluGlu	139

Db 1832 AACCTCCTTTTATGCGGTAATCCGTTGGATCGGTGATCGGCAGCCAGGACTGAATGAAGTG 1891
QY 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513
Db 1892 CTCGCTGGACTGGAACTGGGAAGATGAGTGTGACGGCTGTACGGATGGAACCTTCAGAGGC 1951
QY 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533
Db 1952 ACTCGGTATTTACCTGTGCCCTGAAGAAGCGCTGTTTGGAAACTGAAGAGCTGCAGG 2011
QY 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluAlaGlyCysAsnSer 553
Db 2012 CCTGACTCTAGTTGTCATTCATTCAGCCGGTTTCCATCAGATTGAGCGCTGTAACCTCT 2071
QY 554 LeuAlaPheGlyGlyTyrLeuSerGluValGluGluAsnThrProProLysMetGlu 573
Db 2072 TTAGCAATTTGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAA 2131
QY 574 LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer 593
Db 2132 AAAGAAGGCTTGGAGATAATGATTGGGAAGAAGAAAGGCATCCAGGGTCAATTACAATTCT 2191
QY 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613
Db 2192 TGTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTATGTTCTGTCTGGACACCTGTG 2251
QY 614 LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633
Db 2252 TTACTTAGACCCAAAGAAAGACGATGTAGATATTATAGTGAACCCAGAGCTACTGT 2311
QY 634 ArgThrGluIleValLeuProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653
Db 2312 AGCACAGAAATGTTAATCTCTGAGAAATATATGATATGTTGTGTGTCACAAAAATATG 2371
QY 654 LysLeuArgLysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLys 673
Db 2372 AAATCAGGAAATACTTGAAGAGGTGGAGCTGCATCAGGATTTACCTCTGAAGAAAA 2431
QY 674 AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693
Db 2432 GATCCTGAGGAATCTTGATATATCTGTTTCATCATATTTTAAGGTAGAACCTTTGCTA 2491
QY 694 LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713
Db 2492 AAAATAAGATCAGCAGTCAAAAGGTACAGATTGTTACTTCTATCAAAATTTTATGGAA 2551
QY 714 LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsn 733
Db 2552 AAAAATGAGAAAGTTGCGCGTTCCCAAAATTCAGCAGTTGTAGAATGGTCTTTTATCAAC 2611
QY 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753
Db 2612 AGTAACTGAAATTTGAGGGCACCATCATGCTGATTAATCAGATGCTCCGATTGGA 2671
QY 754 LysAspPheLysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
Db 2672 AAAGACTTTAAACTATTAAAAAAATTTTCTTCTCTGGAATTAATAACAGATTTA 2731
QY 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
Db 2732 CTTGAAGACATCCACAGACGTCCCGATATGTGGAGGGCTTGCAATGTATGATGTAGA 2791
QY 794 GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813
Db 2792 GAATGCTACGACCATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTTGTAAAAACCTGC 2851
QY 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
Db 2852 AACACTCAAGTCCACCTTATCCGAAGAGGCTGAATCATAAATATTAACCCAGGTGTCATT 2911
QY 834 ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu 853
Db 2912 CCCAAAGACTTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGGCAGATATGGAG 2971

QY 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
Db 2972 TTAATTTGCTGTTCTGTCATAGAAACAAGCACAATATGTTGCTTTTGTGAAGTATGGAAG 3031
QY 874 AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893
Db 3032 GACGATTTCTGCTGGCTCTTCTTTGACAGCATGGCCGATCGCGATGGTGGTGCAGAAATGCC 3091
QY 894 PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913
Db 3092 TTCAACATTTCTCAAGTCACCCATGCCAGAGATGAGAGAGTACTTTGAAGATGCTCTCG 3151
QY 914 GluAspLeuHisSerLeuAspSerArgIleGlnGlyCysAlaArgArgLeuLeuCys 933
Db 3152 GAAGACCTGCATTCCTTGGACTCCAGAGAAATCCAAGCTGTGCAGGAAGACTGCTTTGT 3211
QY 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3212 GATCATATATGTGCATGTACCAGATGCCAACAAATGAGTTGTACAAA 3259

RESULT 25

US-60-324-185-23812

; Sequence 23812, Application US/60324185

; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald

; APPLICANT: Lal, Preeti

; APPLICANT: Diep, Dinh

; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING

; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE

; FILE REFERENCE: POLYMORPHISMS IDENTIFIED THEREBY

; CURRENT APPLICATION NUMBER: US/60/324,185

; CURRENT FILING DATE: 2001-09-21

; NUMBER OF SEQ ID NOS: 35862

; SOFTWARE: PERL Program

; SEQ ID NO 23812

; LENGTH: 6314

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 338326.5

; NAME/KEY: unsure

; LOCATION: 5941

; OTHER INFORMATION: a, t, c, g, or other

US-60-324-185-23812

Alignment Scores:

Pred. No.:	0	Length:	6314
Score:	4970.00	Matches:	945
Percent Similarity:	99.47%	Conservative:	0
Best Local Similarity:	99.47%	Mismatches:	1
Query Match:	98.73%	Indels:	4
DB:	78	Gaps:	4

US-09-671-687A-3 (1-949) x US-60-324-185-23812 (1-6314)

QY 4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db 270 GGCTTATGAGCCCAAGAAAAAGTCACTTCACTTCTGGAAGAGCGGATTTTACITTG 329
QY 24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLysValProLys 43
Db 330 CTTCTTCAAGATGCAGCTTACAGACAAACAAACAAACAAAGCTCTTTAAAGTACCGAAG 389
QY 44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db 390 GGAAGTATAGGACAGATATATTCAAGATCGTTCTGTGGGGCAATCAAGGATTCCTTCTGCA 449
QY 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83
Db 450 AAAGCAAGAAAAATCAGATTGGATTAAAAATTTCTAGGCAACCTCATGCACTTCTCTTT 509

[illegible]

```
Db 2670 GACATCTCAGCTGGAAATAATCAAGCAGTTTTTTGTAATAACCTTGCACACTCAAGTCCACCTT 2729
Qy 820 HisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAsp 839
Db 2730 CATCCGAAGAGGCTGAATCATAATAATAACCCAGTGTCACTTCCCAAGAGCTTACCCGAC 2789
Qy 840 TrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCys 859
Db 2790 TGGGACTGGAGACACCGCTGCATCCCTTGCAGAAATATGGAGTTATTTGCTGTCTCTGC 2849
Qy 860 IleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLeu 879
Db 2850 ATGAAACCAAGCCACTATGTCTTTGTGAAGTATGGAGAGCAGATCTCGCTCGCTC 2909
Qy 880 PhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVal 899
Db 2910 TTCTTTGACAGCATGCGCATCGGATGGTGTGTCAGAAATGGCTTCAACATTCCTCAAGTC 2969
Qy 900 ThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLeu 919
Db 2970 ACCCATGCCCCAGAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTG 3029
Qy 920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMet 939
Db 3030 GACTCTCAGGAGAAATCCAAAGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGCATG 3089
Qy 940 TyrGlnSerProThrMetSerLeuTyrLys 949
Db 3090 TACCAGAGTCCCAACATGATTTGTACAAA 3119

RESULT 26
US-60-213-359-5981
; Sequence 5981, Application US/60213359
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lai, Preeti
; TITLE OF INVENTION: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; TITLE OF INVENTION: Identified Thereby
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 5981
; LENGTH: 6315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 338326.5
; NAME/KEY: unsure
; LOCATION: 5942
; OTHER INFORMATION: a, t, c, g, or other
US-60-213-359-5981

Alignment Scores:
Pred. No.: 0 Length: 6315
Score: 4953.00 Matches: 944
Percent Similarity: 99.26% Conservative: 0
Best Local Similarity: 99.26% Mismatches: 2
Query Match: 98.39% Indels: 5
DB: 76 Gaps: 4

US-09-671-687A-3 (1-949) x US-60-213-359-5981 (1-6315)

Qy 4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db 270 GCGTTATGAGCCAGAAAAGTCACTTCACCCCTACTGGGAAGAGCGGATTTTTTACTTG 329
Qy 24 LeuLeuGlnGluCysSerValThrAspLysGlnThrLysLeuLeuLysValProLys 43
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Db 330 CTTCTTCAAGAAATGCAGGTTTACAGACAAACAAACACAAAAGCTCCTTTAAAGTACCGAAG 389
Qy 44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db 390 GGAAGTATAGACAGTATATTTCAAGATCGTTCTGTGGGGCATTTCAAGGATTCCTTCTGCA 449
Qy 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83
Db 450 AAAGCAAGAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCGATTCTCTTT 509
Qy 84 ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuAlaIle 102
Db 510 GTTGATGAAAAGGATGTTGTAGACATAAATGAAAAGTTTACAGAGATTACTTTTGGCAATT 569
Qy 103 ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnAtqLeuSerLysGlyLeu 122
Db 570 ACCAATTGTGAGGAGAGGTTGAGCTGTTTAAAACAGAAAACAGACTTAAGTAAGCCCTC 629
Qy 123 GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePro 142
Db 630 CAAATAGACGTGGGCTGTCTGTGAAAAGTACAGCTGAGATCTGGGGAAGAAAAATTCCT 689
Qy 143 GlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePhe 162
Db 690 GGAAGTTGTACGCTTACAGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGAATATTCCTT 749
Qy 163 GlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGly 182
Db 750 GGAAGTTGAAATTCCTGGGAAGAGGTCGTGGTCAAGGTTTCACTGACGGGGTGTACCAAGGG 809
Qy 183 LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu 201
Db 810 AAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTGTCATTGGACAAGCTAGAA 869
Qy 202 LeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet 221
Db 870 CTCATAGAGATGATGACATCTGCACTTGGAAAGTGATTACGCAGGTCCTCGGACACAATG 929
Qy 222 GlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyLysThr 241
Db 930 CAGGTCGAATCTCTCTCTTGGAAATAAATCCAGAGTTTCTTTGAAGGTTGGAGAAACA 989
Qy 242 IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr 261
Db 990 ATAGAATCTGGAACAGTTATTTCTGTGATGTTTTCAGGAAAGAAAGAAAGCTTAGGATAT 1049
Qy 262 PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal 281
Db 1050 TTTGTTGGTGTGCACATGGATAACCCCTATTGGCAACTGGGATGGAAGATTTGATGGAGTG 1109
Qy 282 ---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle 300
Db 1110 CAGCTTTGTAGTTTTCGCTGTGTTGAAAGTACAAATCTTATTGGACATCAATGATATCATC 1169
Qy 301 ProGluSerValThrGlnGluArgArgProLysLeuAlaPheMetSerArgGlyVal 320
Db 1170 CCAGAGAGTGTGACGAGGAAGAGGCCCTCCCAAACTTGCCTTTATGTCAAGAGGTGT 1229
Qy 321 GlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro 340
Db 1230 GGGGCAAGAGTTTCATCCACTATAATAAACCAAGGCTACAGGATCTACCTCAGACCCT 1289
Qy 341 GlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGln 359
Db 1290 GGAATAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTTCTGTTGACTCACAA 1349
Qy 360 ProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAspProAlaLys 379
Db 1350 CCACAAATCCAAATCAAAAAATACATTGATGAAGTTGCAGAGACCCCTGCACAAA 1409
Qy 380 SerLeuThrGluIleSerThrAspPheAspArgSerProProLeuGlnProProPro 399
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Db 1410 TCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTCCACACACCTCCAGCCTCTCCT 1469
Qy 400 ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet 419
Db 1470 GTGAACCTCACTGACACCGAGAGACAGATTCCACTCTTTACCATTCAGTCTCACCAAGATG 1529
Qy 420 ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet 439
Db 1530 CCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGTGAGCCAGTCTGTAATG 1589
Qy 440 GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn 459
Db 1590 GAAGAGCTAAACACTGCACCCGTCGAAGAGAGTCCACCTTGGCCATGSCCTCTCTGGGAAC 1649
Qy 460 SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGly 479
Db 1650 TCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCTCTCTATGGG 1709
Qy 480 ValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu 499
Db 1710 GTAATCCGTGGATCGGTACGCCACACAGGACTGAATGAAGTGTCTCGTGGACTGGAACGTG 1769
Qy 500 GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys 519
Db 1770 GAAGATGAGTGTGCGAGCTGTAGCGATGGAACCTTCAGAGGCACCTCGGTATTTTCACTGT 1829
Qy 520 AlaLeuLysAlaLeuPheValLysLeuLysSerCysArgProAspSerArgPheAla 539
Db 1830 GCCCTGAAGAAGCGCTGTTTGTGAACCTGAAGAGCTGCAGGCGCTGACTCTAGGTGTGCA 1889
Qy 540 SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeu-AlaPheGlyGlyTy 559
Db 1890 TCATTGACCGCGTTCATTCAGATTGAGCGCTGTAACTCTTTAGGTATTTGGAGGCTA 1949
Qy 559 rLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluIle 579
Db 1950 CTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGMAAAAGAGCGCTTGGAGAT 2009
Qy 579 eMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrIleuAspSerTh 599
Db 2010 AATGATTGGGAAGAAGAGCGATCCAGGCTCATTAACAATTTCTTTACTTAGACTCAAC 2069
Qy 599 rLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysG1 619
Db 2070 CTTATTCTGCTTATTGCTTTAGTCTGTGACACACTGTACTTTAGACCCAAAGA 2129
Qy 619 uLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValas 639
Db 2130 AAAGAACGATGTAGAATATTATAGTGAACCCAGAGCTACTGAGGACAGAAATTTGTTAA 2189
Qy 639 nProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLe 659
Db 2190 TCCTCTGAGAAATATATGATGTGTGTGTCACAAAAATTTATGAACTGAGGAAAAATCT 2249
Qy 659 uGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLe 679
Db 2250 TGAAGAGGTGGAGCTGCATCAGGATTTACTCTGAAGAAAAAGATCCTGAGGAATTTCTT 2309
Qy 679 uAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaG1 699
Db 2310 GAATATTCTTTTCATCATATTTTAAGGTAGAACCTTTTCTAAATAATAGATCAGCAGG 2369
Qy 699 yGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValG1 719
Db 2370 TCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGMAAAAAAATGAGAAAGTTGG 2429
Qy 719 yValProThrIleGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeuLysPheAl 739
Db 2430 CGTTCCCAAAATTCAGCAGTGTGTAGAAATGGTCTTTTATCAACAGTAACCTGAAATTTGC 2489
Qy 739 aGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPheLysLeuPh 759
Db 2490 AGAGGACCAATCATGCTGTATTCAGATGCGCTCGATTGGAAAAAGACTTTAAACTATT 2549

Qy 759 eLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProAr 779
Db 2550 TAAAAAATTTTCTCTCTCGGAATTAATATAACAGATTTACTTTGAAGACACTCCACAG 2609
Qy 779 gGlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPr 799
Db 2610 ACAGTCCGGATATGTGGAGGCTTGCAATGTATGAGTGTAGAGAATGCTACGACGATCC 2669
Qy 799 oAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLe 819
Db 2670 GGACATCTCAGCTGGAATAATCAAGCAGTTTGTAAAAACCTGCACACACTCAAGTCCACCT 2729
Qy 819 uHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAs 839
Db 2730 TCATCCGAAGAGGCTGAATCATATAATATAACCCAGTGTCACTTCCCAAGAGACTTACCCGA 2789
Qy 839 pTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCy 859
Db 2790 CTGGAGCTGGAGACACGGCTGCATCCCTTGCAGAAATATGAGTTATTTGCTGTCTCTG 2849
Qy 859 sIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLe 879
Db 2850 CATAGAAACCAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGGACGATTTCTGCCTGGCT 2909
Qy 879 uPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVa 899
Db 2910 CTTCTTTGACAGCATGCGCGATCGGATGGTGGTCAGAAATGGCTTCAACATTTCTTCAAGT 2969
Qy 899 lThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLe 919
Db 2970 CACCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTTCTTT 3029
Qy 919 uAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMe 939
Db 3030 GGACTCCAGGAGATCCAAAGGCTGTGCACGAAGACTGCTTTGTGATGATATATGTGCAT 3089
Qy 939 tTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3090 GTACCAGAGTCCAAATGAGTTTGTACAAA 3120

RESULT 27

US-60-278-232-7384
; Sequence 7384, Application US/60278232
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0011 P
; CURRENT APPLICATION NUMBER: US/60/278,232
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12,557
; SOFTWARE: PERL Program
; SEQ ID NO 7384
; LENGTH: 6316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 338326.5
; NAME/KEY: unsure
; LOCATION: 5943
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-232-7384

Alignment Scores:
Pred. No.: 0 Length: 6316
Score: 4953.00 Matches: 944
Percent Similarity: 99.26% Conservative: 0
Best Local Similarity: 99.26% Mismatches: 2

Query Match:	98.39%	Indels:	5
DB:	77	Gaps:	4
US-09-671-687A-3 (1-949) x US-60-278-232-7384 (1-6316)			
QY	4	GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu	23
DB	270	GGCTTATGGAGCCCAAGAAAGTCACTTCACTCCCTACTGGGAGAGCGGATTTTACTTG	329
QY	24	LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLysValProLys	43
DB	330	CTTCTTCAAGATGCGAGCGTTACAGACAAACAAACAAAGCTCCTTAAAGTACCGAAG	389
QY	44	GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla	63
DB	390	GGAAATATAGGACAGTATATTCAGATCGTCTGTGGGGCAATTCAGAGATTCTCTGCA	449
QY	64	LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAlaValLeuPhe	83
DB	450	AAAGGCAAGAAANTCAGATTGGATTAAAAATTCAGAGCAACTCATGCAATTCTCTTT	509
QY	84	ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuAlaIle	102
DB	510	GTTGATGAAAAGGATGTTGTAGAGATAAATGAAAGTTACACAGATTACTTTTGGCAATT	569
QY	103	ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeu	122
DB	570	ACCAATTTGTGAGGAGAGGTTACGCTCTTTAAAAAACAGAAACAGACTAAGTAAAGGCTC	629
QY	123	GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePro	142
DB	630	CAAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTCGGGAAAGAAAATTTCT	689
QY	143	GlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePhe	162
DB	690	GGAGTTGTACGCTTCAGAGACCCCTGTTAGCAGAGAGACAGTCTCCGGAATATTCTTT	749
QY	163	GlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGly	182
DB	750	CGAGTTGAATTTCTGGAAGAAGCTCGTGTCAAGGTTTCACTGACGGGTGTACCAAGGG	809
QY	183	LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu	201
DB	810	AAACAGCTTTTTCAGTGTATGAAGATTGTGGCGTGTGTTGTCATTGACAGCTAGAA	869
QY	202	LeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet	221
DB	870	CTCATAGAAGATGATGACACTGCAITGGAAAGTATTACGCGAGTCTCGGGGACACAATG	929
QY	222	GlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyGluThr	241
DB	930	CAGGTGGAATCTCTCTTGGAAATAAATCCAGAGTTTCTTTGAAGGTTGGAGAAACA	989
QY	242	IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr	261
DB	990	ATAGAATCTGGAACAGTTATATCTGTGATGTTTTCGCCAGGAAAAGAAAGCTTAGCAT	1049
QY	262	PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal	281
DB	1050	TTTGTGTGTGCGACATGGATTAACCTATTGTCACACTGGGATGGGAAGATTGATGGAGTG	1109
QY	282	---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle	300
DB	1110	CAGCTTTGTAGTTTGGGTGTGTGAAAGTACAATTCATATGCACATCAATGATATCATC	1169
QY	301	ProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSerArgGlyVal	320
DB	1170	CCAGAGAGTGTGACCGAGGAAAGAGGCTCTCCAAACTTGCCTTTATGTGCAAGAGTGT	1229
QY	321	GlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro	340
DB	1230	GGGCAAAAGGTTTCTCCAGTATAATAAACCAAGGCTACAGGATCTACCTCAGACCT	1289
QY	341	GlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGln	359
DB	1290	GGAAATAGAAACAGACTCTGAATTTATATACCTTAAATGGGTCTTCTGTGACTCACAA	1349
QY	360	ProGlnSerLysSerLysAsnThrTyrTyrIleAspGluValAlaGluAspProAlaLys	379
DB	1350	CCACAAATCCAATCAAAAATACATGTTACATGATGAAGTTGCAGAGACCTTGCAAAA	1409
QY	380	SerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGlnProProPro	399
DB	1410	TCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCCACCACCACTCCAGCTCTCT	1469
QY	400	ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet	419
DB	1470	GTGAACCTCACTGACACCGAGAACAGATTCACCTCTTTTACCATTTCAGTCTCCACCAAG	1529
QY	420	ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet	439
DB	1530	CCCATACCAATGGAGTATTGGCCACAGTCCACTTCTGTGACGCCAGTCTGTGTAATG	1589
QY	440	GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn	459
DB	1590	GAAGAGCTAAACACTGACCCCGTCCAGAGAGTCCACCCTTGGCCATGCTCTGGGAC	1649
QY	460	SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGly	479
DB	1650	TCACATGGCTAGAAAGTGGGCTCATTTGGCTGAAGTAAAGGAGAACCTCTCTTTCTATGG	1709
QY	480	ValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu	499
DB	1710	GTAAATCCGTTGGATCGGTCAGCCACAGACTGAATGAAGTGTCTCGCTGAGCTGGAAC	1769
QY	500	GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys	519
DB	1770	GAAGATGAGTGTGCGAGCTGTGCGATGGAAACCTTCAGAGCACTCGGTATTTTACCTGT	1829
QY	520	AlaLeuLysLysAlaLeuPheValLysSerCysArgProAspSerArgPheAla	539
DB	1830	GCCTGGAAGAAGCGCTGTTTGTGAAACTGAAGAGCTGCAGCGCTGACTCTAGGTTTGA	1889
QY	540	SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeu-AlaPheGlyGlyTyr	559
DB	1890	TCATTGCGCGGTTTCCAAATCAGATTGAGCGCTGTAACTCTTTAGGTATTGAGGCTA	1949
QY	559	rLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluI	579
DB	1950	CTTAAAGTGAAGTAGTAGAAGAAATACTCCACCAAAAATGGAAAAGAGCTTGGAGAT	2009
QY	579	eMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerTh	599
DB	2010	AATGATTGGGAAGAGAAAGGCATCCAGGTCATTACAAATCTTGTACTTTAGACTCAAC	2069
QY	599	rLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysG	619
DB	2070	CTTATTCTGCTTATTTGCTTTTGTCTGTCGACACTGTGTACTTAGACCCAAAGA	2129
QY	619	uLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValAs	639
DB	2130	AAAGAACGATGTAGAATATTATAGTGAACCCCAAGAGCTACTGAGGACAGAAAATGTTAA	2189
QY	639	nProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLe	659
DB	2190	TCCTCTGAGATATATGATATGTGTGTGCCCAAAAATTTATGAATCTGAGAAAAATCT	2249
QY	659	uGluLysValGluAlaAspGlyPheThrSerGluGluLysAspProGluGluPheLe	679
DB	2250	TGAAGAGGTGGAGCTGCATCAGATTACTCTCTGAAGAAAGATCTCTGAGGAATCTT	2309
QY	679	uAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaG	699
DB	2310	GAATATCTGTTTTCATCATATTTTAAAGGGTAGAACCTTTTGTAAAAATAAGATCAGCAG	2369
QY	699	yGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValG	719

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Db 2370 TCAAAAGGTACAGATTGTTACTTCTATCAAAATTTTATCGAAAAAATGAGAAAGTTGG 2429
Qy 719 yValProThrIleGlnLeuLeuGluTTPSerPheIleAsnSerAsnLeuLysPheAl 739
Db 2430 CGTTCACCAANTCAGCAGTGTGTAGAAATGGTCTTTTATCAACAGTAACCTGAAATTTGC 2489
Qy 739 aGluAlaProSerCysLeuIleIleGlnMetProAtgPheGlyLysAspPheLysLeuPh 759
Db 2490 AGAGGCACCATCATGCTGATTATTCAGATGCTCGATTTGGAAAAAGACTTTTAAACTATT 2549
Qy 759 eLysLysIlePheProSerLeuGluLeuAenIleThrAspLeuLeuGluAspThrProAr 779
Db 2550 TAAAAAAATTTTCCCTCTCTCGAAATATAAATAACAGATTTACTTGAAGACACTCCACG 2609
Qy 779 gGlnCysArgIleCysGlyLysLeuAlaMetTyrGluCysArgGluCysTyrAspAspPr 799
Db 2610 ACAGTCCCGGATATGTGAGGGCTTGCAATGTATGATGTAGAGATGTCTACGACGATCC 2669
Qy 799 oAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLe 819
Db 2670 GGACATCTCAGCTGGAATAATCAAGCAGTTTTTGTAAAACTTGCACACTCAAGTCCACCT 2729
Qy 819 uHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAs 839
Db 2730 TCATCCGAGAGGCTGAATCATAAATATAACCCAGTGTCTACTTCCCAAGACTTACCCTGA 2789
Qy 839 pTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCy 859
Db 2790 CTGGGACTGGAGACACCGGCTGCATCCCTTCCGAGAAATATGAGATTATTGCTGTCTCTG 2849
Qy 859 sIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspSerAlaTrpLe 879
Db 2850 CATAGAAACCAAGCCACTATGTGCTTTTGGAAGATGTGGAAGACGATTCTGCCTGGCT 2909
Qy 879 uPhePheAspSerMetAlaAspArgAspGlyGlnAsnGlyPheAsnIleProGlnVa 899
Db 2910 CTTCCTTTGACAGCATGCGCCATCGGGATGTTGTCAGAAATGGCTTCAACATTCTCAAGT 2969
Qy 899 lThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLe 919
Db 2970 CACCCCATGCCAGAGTAGGAGTAGTACTTGAAGATGCTCTGGAAGACCTGCATTCCTT 3029
Qy 919 uAspSerArgIleGlnGlyCysAlaArgAlaArgLeuLeuCysAspAlaTyrMetCysMe 939
Db 3030 GGACTCCAGAGAAATCAAGGCTGTGCACGAAGCTGCTTTGTGATGCATATATGTGCAT 3089
Qy 939 tTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3090 GTACCAGATCCCAACATGAGTTGTACAAA 3120
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RESULT 28

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US-09-786-797B-25
; Sequence 25, Application US/09786797B
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0594 PCT
; CURRENT APPLICATION NUMBER: US/09/786,797B
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 09/156,470; unassigned; 60/131,321
; PRIOR FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27
; NUMBER OF SEQ ID NOS: 32
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; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 4527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2363327
US-09-786-797B-25

Alignment Scores:
Pred. No.: 0 Length: 4527
Score: 4942.00 Matches: 944
Percent Similarity: 99.37% Conservative: 0
Best Local Similarity: 99.37% Mismatches: 2
Query Match: 98.17% Indels: 5
DB: 32 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-786-797B-25 (1-4527)

Qy 4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db 270 GGCTTATGGAGCCCAAGAAAAAGTCACCTTACCCTACTGGGAAGACGGATTTTTTACTTG 329
Qy 24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLysValProLys 43
Db 330 CTCTTCAAGATGTCAGCGTTTACAGACAAACACAAAAGCTCCTTAAAGTACCGAA- 388
Qy 44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db 389 GGAAGTATAGCAGATATATTCAAGATCGTTCGTGGGCATTCAAGGATTCTTCTGCA 448
Qy 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAlaValLeuPhe 83
Db 449 AAAAGCAAGAAAAATCAGATTGGATTAAAAATTTTAGAGCAACCTCATGCAAGTTCTCTTT 508
Qy 84 ValAspGlu--AspValValGluIleAsnGluLysPheThrGluLeuLeuAlaIle 102
Db 509 GTTGATGAAAGGATGTTGTAGATTAATGAAAAGTTTCAGAGTTACTTTTGGCAATT 568
Qy 103 ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeu 122
Db 569 ACCAAATGTCAGGAGAGGTTTCAAGCTGTTTAAAAACAGAAACAGACTTAAGTAAAGGCCTC 628
Qy 123 GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluLysLysPhePro 142
Db 629 CAAATAGACCTGGGCTGCTCTGTGAAAAGTACAGCTGAGATCTGGGGAAGAAAAATTTCT 688
Qy 143 GlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePhe 162
Db 689 GGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGCAGCTCTCCGGAATATTCTTT 748
Qy 163 GlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGly 182
Db 749 GGAGTTGAATTGCTGGGAAGAGGTCGTGTTCAAGGTTTCACTACGGGGGTGTACCAAGG 808
Qy 183 LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu 201
Db 809 AAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGCTGTTTGTGCAATTGGCAAGCTAGAA 868
Qy 202 LeuIleGluAspAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet 221
Db 869 CTCATAGAAGATGATGACACTGTCATTGGAAGTGAATACGAGGTCCTGGGGACACAATG 928
Qy 222 GlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGlyGlyGluThr 241
Db 929 CAGTCCAACTTCTCTCTTGGAAATAAACTCCAGAGTTTCTTGAAGGTTGGAGAAACA 988
Qy 242 IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr 261
Db 989 ATAGAACTCGAACAGTTATATTCTGTGATGTTTTTGCAGGAAAAAGAAAGCTTAGGATAT 1048
Qy 262 PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal 281
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|||||
1049 TTTGTTGGTGGACATGGATTAACCCCTATTGGCAACTGGGATGGAAGATTGATGGAGTG 1108
QY 282 ---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle 300
Db 1109 CAGCTTTGTAGTTTGGTGTGTTGAAAGTACAAATTCATTGGCACATCAATGATATCATC 1168
QY 301 ProGluSerValThrGlnGluArgProProLysIleAlaPheMetSerArgGlyVal 320
Db 1169 CCAGAGAGTGTGACGAGGAAAGGAGGCTCCCAAACTTGGCTTTATGTCAAGAGGTGTT 1228
QY 321 GlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro 340
Db 1229 GGGACAAAGGTTTCATCCAGTCATAATAACCAAGGCTACAGGATCTTACCCTCAGACCC 1288
QY 341 GlyAsnArg---ArgSerGluLeuPhePheThrLeuAsnGlySerSerValAspSerGln 359
Db 1289 GGAATAGAAACAGATCTGAATATTATTTATACCTTAATGGGTCTTCTGTGTACTCAAA 1348
QY 360 ProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAspProAlaLys 379
Db 1349 CCACAATCCAAATCAAAAAATACATGTGATGAAAGTTGCAGAAGACCCCTGCAAAA 1408
QY 380 SerLeuThrGluIleSerThrAspPheAspArgSerProProLeuGlnProProPro 399
Db 1409 TCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCCACCACACTCCAGCCCTCCT 1468
QY 400 ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet 419
Db 1469 GTGACTACTGACCCAGGAGAACAGATTCCACTCTTTACATTCAGTCTCACCAGATG 1528
QY 420 ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet 439
Db 1529 CCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTGTCTGACGCCAGTCTGTAATG 1588
QY 440 GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn 459
Db 1589 GAAGAGCTAAACACTGCACCGCTCCAAAGAGAGTCCACCTTGGCCATGCTCTCTGGGAAC 1648
QY 460 SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPheThrGly 479
Db 1649 TCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCTTCTATGGG 1708
QY 480 ValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu 499
Db 1709 GTAAATCCGTGGATCGGTGACCCACAGGACTGAAAGTGAAGTGAAGGAGAACCTCTCTTCTATGGG 1768
QY 500 GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys 519
Db 1769 GAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTATTTTCACTGT 1828
QY 520 AlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSerArgPheAla 539
Db 1829 GCCCTGAAGAAGCGCTGTTGTGAAACTGAAGAGCTGCGAGGCTGACTCTAGGTTTGGCA 1888
QY 540 SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyTyr 559
Db 1889 TCATTGAGCGGTTTCCATCAGATTGAGCGCTGTAACCTTTAGCATTTTGGAGGCTAC 1948
QY 560 LeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluIle 579
Db 1949 TTAAGTGAAGTAGTAGAAGAAATACCTCCACCAAAATGAAAAGAGAGGCTGGAGATA 2008
QY 580 MetIleGlyLysLysLysGlyIleGlnGlyHisThrAsnSerCysTyrLeuAspSerThr 599
Db 2009 ATGATTGGGAAGAAAGAGCATCCAGGTCATTACAAATCTTGTACTTAGACTCAACC 2068
QY 600 LeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysGlu 619
Db 2069 TTAATCTGCTATTTGCTTTTAGTCTGTGACACTGTGTACTTAGACCCCAAGAA 2128
QY 620 LysAsnAspValGluTyrTyrSerGluThrGlnLeuLeuArgThrGluIleValAsn 639
|||||

Db 2129 AAGAACGATGTAGAAATATTATAGTGAAACCCAGAGCTACTGAGGACAGAAATTGTAAT 2188
QY 640 ProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLeu 659
Db 2189 CCTCTGAGAAATATATGGATATGTGTGCCACAAAAATATGAACTGAGGAAAAATACCT 2248
QY 660 GluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLeu 679
Db 2249 GAAAAGGTGGAGGCTGCATCAGGATTTTACCTCTGAAGAAAAAGATCCTGAGGAATTTCTTG 2308
QY 680 AsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaGly 699
Db 2309 AATATTCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTAAAAATAAGATCAGCAGGT 2368
QY 700 GlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGly 719
Db 2369 CAAAAGGTACAGATTTGTTACTTCTATCAATTTTTATGAAAAAAAATCGAAAAAGTTGGC 2428
QY 720 ValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeuLysPheAla 739
Db 2429 GTTCCCACAATTCAGCAGTTGTTAGATGGTCTTTTATCAACAGATAACCTGAAATTTGCA 2488
QY 740 GluAlaProSerCysLeuIleGlnMetProArgPheGlyLysAspPheLysLeuPhe 759
Db 2489 GAGGACCATCATGTCTGATTATTAGATTCGCTCGATTTGGAAAAAGACTTTAAACTATTT 2548
QY 760 LysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProArg 779
Db 2549 AAAAAATTTTCTCTCTGGAATTAATAATAACAGATTTACTTGAAGACACTCCACGA 2608
QY 780 GlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPro 799
Db 2609 CAGTGCCGATATCTGGAGGCTTGTCAATGATGATGATGATGATGATGATGATGATGATG 2668
QY 800 AspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLeu 819
Db 2669 GACATCTCAGCTGAAAAAATCAAGCAGTTTGTGTAACCTGCAACACTCAAGTCCACCTT 2728
QY 820 HisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAsp 839
Db 2729 CATCCGAAGAGCTGGAATCATATAATCAACCCAGTGTCACTTCCCAAGACTTACCCGAC 2788
QY 840 TrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCys 859
Db 2789 TGGGACTGGAGACACGCTGCATCCCTTGCAGAAATATGAGATTATTTGCTGTTCTCTGC 2848
QY 860 IleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLeu 879
Db 2849 ATAGAAAACAGCCACTATGTTGCTTTGTGAAGTATGGAAGGACGATTTGCTCTGGCTC 2908
QY 880 PhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVal 899
Db 2909 TTTCTTTACAGCATGGCCGATCGGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2968
QY 900 ThrProCysProGluValGlyGlyTyrLeuLysMetSerLeuGluAspLeuHisSerLeu 919
Db 2969 ACCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGAGACTGATTCCTTG 3028
QY 920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMet 939
Db 3029 GACTCCAGGAGATCCCAAGGCTGTGCAGGAAGACTGCTTTGTGATGCATATATGTGCATG 3088
QY 940 TyrGlnSerProThrMetSerLeuTyrLys 949
Db 3089 TACCAGAGTCCAAATCAGTGTGTACAAA 3118

RESULT 29

US-10-921-707-25
; Sequence 25, Application US/10921707
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom

APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: BANDMAN, Olga
APPLICANT: CORLEY, Neil C.
APPLICANT: GUEGLER, Karl J.
APPLICANT: PATTERSON, Chandra
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS
FILE REFERENCE: PF-0594 PCT
CURRENT APPLICATION NUMBER: US/10/921,707
CURRENT FILING DATE: 2004-08-19
PRIOR APPLICATION NUMBER: US/09/786,797
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 09/156,470; unassigned; 60/131,321
PRIOR FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 4527
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 2363327
US-10-921-707-25

Alignment Scores:
Pred. No.: 0 Length: 4527
Score: 4942.00 Matches: 944
Percent Similarity: 99.37% Conservative: 2
Best Local Similarity: 99.37% Mismatches: 0
Query Match: 98.17% Indels: 5
DB: 63 Gaps: 4

US-09-671-687A-3 (1-949) x US-10-921-707-25 (1-4527)

QY 4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db 270 GGCTTATGGAGCCAAAGAAAGTACATTCACCTTACTGGGAGAGCGGATTTTTTACTTG 329

QY 24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLysValProLys 43
Db 330 CTTCCTCAAGATGCAGCGTTACAGACAAACAAACAAAGCTCCTTAAAGTACCGAA - 388

QY 44 GlySerIleGlyInTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db 389 GGAAGTATAGGACAGATATATCAAGATCGTTCTGTGGGGCATTCAAGGATTCCTCTGCA 448

QY 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83
Db 449 AAAGGCAAGAAATACAGTTGGATTAAAAATTTAGAGCAACCTCATGCGATTCCTCTTT 508

QY 84 ValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeuAlaIle 102
Db 509 GTTGATGAAAGGATGTTGTAGATATAATGAAAGTTTCAAGAGTTACTTTTGGCAATT 568

QY 103 ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeu 122
Db 569 ACCAATTTGAGGAGAGGTTGAGCTGTTTAAAAACAGAAACAGACATAAGTAAAGGCGCT 628

QY 123 GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePro 142
Db 629 CAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAATTTCTCT 688

QY 143 GlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePhe 162
Db 689 GGAGTTGTACGCTTCAGAGGACCCCTGTTACAGAGGACAGCTCTCCGGAATATCTTT 748

QY 163 GlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyValTyrGlnGly 182
Db 749 GGAGTTGAAATGCTGGAAGAGGTCGTGGTCAAGGTTTCACTGACGGGGTGTACCAAGGG 808

QY 183 LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu 201
Db 809 AAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTGCTTGCATTCGCAAGCTAGAA 868

QY 202 LeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet 221
Db 869 CTCATGAAGATGATGACATGCAATGGAAAGTGAATACCGCAGGTCCTGGGACCAATG 928

QY 222 GlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyGluThr 241
Db 929 CAGTCTGAACCTTCTCTTTGGAATAAATCTCCAGAGTTTCTTTGAAGGTTGGAGNACA 988

QY 242 IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr 261
Db 989 ATGAATCTGGAACAGTTATATTTCTGTGATGTTTTTCCAGGAAAGAAAGCTTAGGATAT 1048

QY 262 PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal 281
Db 1049 TTTCTGTGTGGACATGGATAACCTTATTTGGCAATCGGATGGAGATTTTGTATGGAGTG 1108

QY 282 ---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle 300
Db 1109 CAGCTTTGTAGTTTTGCGTGTGTTGAAAGTACAATCTTATTCACATCAATGATATCATC 1168

QY 301 ProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSerArgGlyVal 320
Db 1169 CCAGAGATGTGACGACGAGAAAGGAGGCTCTCCAAACTTGCCTTTATGTCAAGAGGTGT 1228

QY 321 GlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro 340
Db 1229 GGGGACAAAGGTTTCATCCAGTCAATAAATAACAAAGGCTACAGGATCTACCTCAGACCT 1288

QY 341 GlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGln 359
Db 1289 GGAATAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTTCTGTTGACTCACAA 1348

QY 360 ProGlnSerLysSerLysAsnThrTyrIleAspGluValAlaGluAspProAlaLys 379
Db 1349 CCACATCCAAATCAAAAATACATGTTACATGATGAATGTCAGAGACCTTCGCAAAA 1408

QY 380 SerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGlnProProPro 399
Db 1409 TCTCTTACAGAGATATCTACAGACTTTCAGCGCTTCTTACCACCACTTCAGGCTCTCTCT 1468

QY 400 ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet 419
Db 1469 GTGAACCTACCTGACCCACCGAAGACAGATTCACCTTTTACCATTGCTCTCAGGATG 1528

QY 420 ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet 439
Db 1529 CCCAATACCAATGGAGTATTGGCCACAGTCCACTTTTCTGTCTGAGCCAGTCTGTAATG 1588

QY 440 GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn 459
Db 1589 GAAGAGCTAAACACTGCACCCGTCACAGAGAGTCCACCCCTGGCCATGCTCTCTGGGAA 1648

QY 460 SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGly 479
Db 1649 TCACATGCTTAGAAGTGGGCTCATTTGGCTGAAGTTAAAGGAGAACCTCTCTTTCTATGG 1708

QY 480 ValIleArgTyrIleGlyGlnProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu 499
Db 1709 GTAATCCGTTGGATCGGTCCAGCCACAGACTGAATGAAGTCTGCTGGAGCTGGAACTG 1768

QY 500 GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys 519
Db 1769 GAAGATGATGTGCGAGGCTGTACGGATGGAACCTTTCAGAGGCACCTCGGTATTTCACCTGT 1828

QY 520 AlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSerArgPheAla 539
Db 1829 GCCCTGAAAGAGGCGCTGTTTGTGAACACTGAAGAGCTGCAGGCGCTGACTCTAGGTTTGA 1888

QY 540 SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyTyr 559


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Db      1889 TCATTGAGCGGTTTCCAAATCAGATTGAGCGCTGTAACTCTTTAGCATTTTGGAGGCTAC 1948
Qy      560 LeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluIle 579
Db      1949 TTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAGAGGCTTGGAGATA 2008
Qy      580 MetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerThr 599
Db      2009 ATGATTGGGAAGAAGAAGCATCCAGGTCATTACAAATTCCTTGTTACTTAGACTCAACC 2068
Qy      600 LeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysGlu 619
Db      2069 TTAATTCGTCTATTGCTTTTAGTTCTGTGTCGACACTGTGTACTTAGACCCAAAGAA 2128
Qy      620 LysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValAsn 639
Db      2129 AAGAACGATGATAGATATATATAGTAAACCCAGAGCTACTGAGACAGAAATTTGTTAAT 2188
Qy      640 ProLeuArgIleTyrGlyTyrValCysAlaThrIlysIleMetLysLysLeuArgLysIleLeu 659
Db      2189 CCTCTGAGAAATATATGATATGTGTGCCACAAAATTTATGAACTGAGGAAAATACTT 2248
Qy      660 GluLysValGluAlaIaSerGlyPheThrSerGluLysAspProGluGluPheLeu 679
Db      2249 GAAAAGGTGGAGCTGCATCAGGATTTACCTCTCAAGAAAAAGATCCTGAGGAATCTTGT 2308
Qy      680 AsnIleLeuPheHisIleLeuAqValGluProLeuLeuLysIleArgSerAlaGly 699
Db      2309 AATATTCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTAAAAATPAGATCAGCAGGT 2368
Qy      700 GlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGly 719
Db      2369 CAAAAGGTACAGATTGTTACTTCTATCAATTTTATGGAATAATGAGAAAGTTGGC 2428
Qy      720 ValProThrIleGlnGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeuLysPheAla 739
Db      2429 GTTCCACCAATTCAGCAGTTGTTAGAAATGCTTTTATCAACAGTAACCTGAAATTTGCA 2488
Qy      740 GluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPheLysLeuPhe 759
Db      2489 GAGGCACCATCATGTCGATTATTTCAGATGCCCTCGATTTGGAAGAGACTTTAAACTATTT 2548
Qy      760 LysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProArg 779
Db      2549 AAAAAATTTTCTCTCTGGAATTAATATATACAGATTTATTTGAAAGACATCCCGA 2608
Qy      780 GlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPro 799
Db      2609 CAGTGCAGATATGTGGAGGCTTGCAATGATGAGTGTAGAGAAATGCTACGACGATCCG 2668
Qy      800 AspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLeu 819
Db      2669 GACATCTCAGCTGGAATAATCAAGCAGTTTGTAAAAACCTGCAACACTCAAGTCCACCTT 2728
Qy      820 HisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAsp 839
Db      2729 CATCCGAGAGGCTGAATCATAAATAATACCAAGTGTCTTCCCAAGAGACTTACCCGAC 2788
Qy      840 TrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCys 859
Db      2789 TGGGACTGGAGACACGGCTGCATCCCTGCCAGAAATAGAGTTATTTGCTGTCTCTGC 2848
Qy      860 IleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLeu 879
Db      2849 ATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGACGATTTCTGCTGGCTC 2908
Qy      880 PhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVal 899
Db      2909 TTTCTTTGACAGCATGGCCCATGGGATGGTGGTTCAGAAATGGCTTCAACATTCCTCAAGTC 2968
Qy      900 ThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLeu 919
```

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Db      2969 ACCCATGCCCAGAAAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTG 3028
Qy      920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMet 939
Db      3029 GACTCCAGGAGATCCCAAGGCTGTGCACGAAGACTGCTTTTGATGCATATATATGTGATG 3088
Qy      940 TyrGlnSerProThrMetSerLeuTyrLys 949
Db      3089 TACCAGAGTCCACAATGAGTTGTACAAA 3118

RESULT 30
US-60-131-321-21
; Sequence 21, Application US/60131321
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Yue, Henry
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Azimzai, Valda
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN CYTOSKELETAL PROTEINS
; FILE REFERENCE: PF-0692 P
; CURRENT APPLICATION NUMBER: US/60/131.321
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 4527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2363327
US-60-131-321-21

Alignment Scores:
Pred. No.: 0 Length: 4527
Score: 0 942.00 Matches: 944
Percent Similarity: 99.37% Conservative: 0
Best Local Similarity: 99.37% Mismatches: 2
Query Match: 98.17% Indels: 5
DB: 75 Gaps: 4

US-09-671-687A-3 (1-949) x US-60-131-321-21 (1-4527)

Qy      4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db      270 GGCTTATGGAGCCCAAGAAAAAGTCACTTCACTTGGGAAGAGCGGATTTTACTTTG 329
Qy      24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLysValProLys 43
Db      330 CTTCTTCAAGAATGCAGCGTTTACAGAACAAACAAACAAAAAGCTCTTTAAAGTACCGAA- 388
Qy      44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db      389 GGAAGTATAGACAGATATATTTCAAGATCGTCTCTGGGGCATTTCAAGATTTCTTCTGCA 448
Qy      64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83
Db      449 AAAGGCCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCAGTTCCTCTT 508
Qy      84 ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuAlaIle 102
Db      509 GTTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTACAGAGTTTACTTTTGGCAATT 568
Qy      103 ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeu 122
Db      569 ACCAATTGTAGGAGAGGTTTCAGGCTGTTTAAAAACAGAAACAGACTTAAGTAAAGGCTC 628
Qy      123 GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluLysPhePro 142
Db      629 CAAATAGACGTGGGCTGTCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAAAATTTCT 688
```



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Db      2849 ATAGAAACAGCCACTATGTTGCTTTTGTGAGTATGGGAAGGACGATTCTGCCTGGCTC 2908
Qy      880 PhePheAspSerMetAlaAspArgAspGlyGlnAsnGlyPheAsnIleProGlnVal 899
Db      2909 TTCTTTGACAGCATGGCCGATCGGATGGTGGTCTGAGAAATGGCTTCAACATTTCTTCAAGTC 2968
Qy      900 ThrProCysProGluValGlyGlyLeuIleGlyMetSerLeuGluAspLeuHisSerLeu 919
Db      2969 ACCCCATGCCAGAAAGTAGGAGATGACTTGAAGATGCTCTGGGAAGACCTGCAATTCCTTG 3028
Qy      920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaIleTyrMetCysMet 939
Db      3029 GACTCCAGGAGATCCAAAGCTGTGCAGAGACTGCTTTGTGATGCAATATATGTCATG 3088
Qy      940 TyrGlnSerProThrMetSerLeuTyrLys 949
Db      3089 TACCAGAGTCCAAACATGAGTTTGACAAA 3118

RESULT 31
US-60-172-360-22693
; Sequence 22693, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Deep, Dinu
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 22693
; LENGTH: 6315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 338326.5
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5942
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-360-22693

Alignment Scores:
Pred. No.: 0 Length: 6315
Score: 4916.00 Matches: 944
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 2
Query Match: 97.66% Indels: 7
DB: 75 Gaps: 4

US-09-671-687A-3 (1-949) x US-60-172-360-22693 (1-6315)
Qy      4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db      270 GGCTTATGGAGCCAAAGAAAGTCACTTCACCTTACTGGGAAGCGGATTTTATCTTG 329
Qy      24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLysValProLys 43
Db      330 CTTCCTCAAGATGCGAGCTTACAGACAAACAAACAAAGCTCTTAAAGTACCGAA- 388
Qy      44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db      389 GGAAGTAGTAGGACAGTATATTCAGATCGTCTGTGGGGCATTCAGGATTCCTTCTGCA 448
Qy      64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83
Db      449 AAAGGCAAGAAAAATCAGATTGGATTAAAAATTCTAGAGCAACCTCATGCAAGTTCTCTTT 508
Qy      84 ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuLeu-AlaIle 102
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Db      509 GTTGATGAAAGGATGTTGTAGAGATAAATGAAAAAGTTCAACAGAGTTACTTTTGGGCAAT 568
Qy      102 eThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLe 122
Db      569 TACCAATTTGTGAGGAGAGTTTCAGCTCTGTTAAAAACAGAAACAGACAGTAAGTAAAGSCCT 628
Qy      122 uGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePr 142
Db      629 CCAATAGACGTGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAGAAAAATTTCC 688
Qy      142 oGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePh 162
Db      689 TGGAGTTGTGCGCTTCAGAGGACCCCTGTTAGCAGAGAGCAGATCTCCGGAATATTCTT 748
Qy      162 eGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnG 182
Db      749 TGGAGTTGAATTTGCTGGAAGAGGTCTGTGTCAGGTTTCACTGACGGGTGTACCAAG 808
Qy      182 YLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuG 201
Db      809 GAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTGCAATTGGACAAGCTAGA 868
Qy      201 uLeuIleGluAspAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMe 221
Db      869 ACTCATAGAAAGATGATGACACTGCATTGGAAAGTGAATACCGAGGTCTCTGGGGACACAAT 928
Qy      221 tGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyGluPh 241
Db      929 GCAGTGCAACTTCTCTTTGGAAATAAATCTCCAGAGTTTCTTTGAAGTTGGAGAAAC 988
Qy      241 rIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTy 261
Db      989 AATAGAATCTGGAACAGTTATATTCTGTGATGTTTTCAGGAAAAAGAAAGCTTAGGATA 1048
Qy      261 rPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVa 281
Db      1049 TTTTGTGTTGGTGTGACATGGATAACCCCTATTGGCAACTGGGATGGAAGATTGTGAGT 1108
Qy      281 l---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleI 300
Db      1109 GCAGCTTTGTAGTTTTCGCTGTGTGAAAGTACAAATCTATTGCAATCAATGATATCAT 1168
Qy      300 eProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSerArgGlyVa 320
Db      1169 CCCAGAGAGTGTGACGAGGAAAGAGGCGCTCCCAACTTTCCTTTATGTCAAGAGTGT 1228
Qy      320 lGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThrSerAspPr 340
Db      1229 TGGGGACAAAGGTTTCATCCAGTCAATAATAAACCAAGGCTACAGGATCTACCTCAGACC 1288
Qy      340 oGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGl 359
Db      1289 TGGAAATAGAAACAGATCTGAATATTATTATACCTTAATGGGTCTTCTGTGACTACA 1348
Qy      359 nProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAspPro-AlaAl 379
Db      1349 ACCCAATCCAAATCAAAAAATACATGTGATCATTTGTAAGTTGCAAGAGACCTTGGCA 1408
Qy      379 ySerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGlnProProP 399
Db      1409 AATCTCTTACAGAGATATCTACAGACTTGTACCGTCTTCTTCCACCACCTCCAGGCTCTC 1468
Qy      399 roValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysM 419
Db      1469 CTGTGAATCTCACTGACCACCGAGAACAGATTCCTCACTCTTTACCATTCAGTCTCCACAA 1528
Qy      419 etProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValM 439
Db      1529 TGCCCAATACCAATGGAAGATATTGGCCACAGTCCACTTTCTCTGTGACCCAGTCTGTAA 1588
Qy      439 etGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyA 459
Db      1589 TGGNAGAGCTAAACACTGACCCCGTCCNAGAGAGTCCACCTTGGCCATGCTCTCTGGGA 1648
```

Qy 459 snSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrG 479
Db 1649 ACTCACATGGTCTAGAGAGTGGCTCATTTGGCTGAAGTAAAGGAGACCCCTCTTCTATG 1708
Qy 479 lyValIleArgTTPilleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluL 499
Db 1709 GGGTAATCCGTTGGATCGGTGAGCCAGCCAGGACTGAATGAAGTGGCTGGCTGGAGAAC 1768
Qy 499 euGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrC 519
Db 1769 TGAAGATGAGTGGAGGCTGTACCGATGGAACCTTCAGAGGCACTCGGTATTTTCACCT 1828
Qy 519 yAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSerArgPheA 539
Db 1829 GTGCCCTGAAGAGCGCTGTTTGTGAACCTGAAGAGCTGAGAGGCTCTAGGTGTTG 1888
Qy 539 laSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyT 559
Db 1889 CATCATTTGCAGCGGTTTCCAAATCAGATTGAGCGCTGTAACTCTTTAGCATTTGGAGCT 1948
Qy 559 yLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluI 579
Db 1949 ACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAGAGAGGCTTGGAGA 2008
Qy 579 leMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerT 599
Db 2009 TAATGATTGGAGAGAGAGGCAATCCAGGCTCAATCAATCTCTGTACTTTAGACTCAA 2068
Qy 599 hrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysG 619
Db 2069 CCTTATTTCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTGTACTTAGACCCAAAG 2128
Qy 619 lylsAsnAppValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleVala 639
Db 2129 AAAAGAACGATGTAGAATATTATATAGTGAACCCAGAGCTACTCAGGACAGAGAAATGTTA 2188
Qy 639 snProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleL 659
Db 2189 ATCTCTGAGAAATATATGGATATGTGTGTGTCACAAAAATTTATGAATCTGGAGAAATAC 2248
Qy 659 euGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGluGluPheL 679
Db 2249 TTGAAGAGTGGAGCTGCATCAGATTACTCTGAAGAAAGATCTCTGAGGAATCT 2308
Qy 679 euAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerIaG 699
Db 2309 TGAATATCTCTTCATCATATTTTAAGGGTAGAACCTTTGCTAAAAAATAAGATCAGCAG 2368
Qy 699 lyGlnLysValGluAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValG 719
Db 2369 GTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAAAAAATGAGAAAGTTG 2428
Qy 719 lyValProThrIleGlnGlnLeuLeuGluTTPSerPheIleAsnSerAsnLeuLysPheA 739
Db 2429 CGGTTCCACAAATTCAGCAGTTGTAGATGCTCTTTTATCAACAGTAACTCTGAATTTG 2488
Qy 739 laGluAlaProSerCysLeuIleleGlnMetProArgPheGlyLysAspPheLysLeuP 759
Db 2489 CAGAGGCACCATCATGCTGATATTTCAGATGCTCGATTTTGGAAAAAGACTTTAAACTAT 2548
Qy 759 helysLysIlePheProSerLeuGluIleuAsnIleThrAspLeuLeuGluAspThrProA 779
Db 2549 TTAATAAAATTTTCTCTCTGGAATTAATAATATAACAGATTTTACTTTGAAGACACTCCCA 2608
Qy 779 rgGlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspP 799
Db 2609 GACAGTCCCGATATGTGGAGGGCTTGCATATGTATGAGTGTAGAGATGCTTACGACGATC 2668
Qy 799 roAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisL 819
Db 2669 CGGACATCTCAGCTGGAAAAATCAAGCAGATTTTGTGAAAACTGCAACACTCAAGTCCACC 2728

Qy 819 euHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProA 839
Db 2729 TTCAATCCGAGAGGCTGAATCATAAATATAAACCAGTGTCACTTCCCAAGACTTTACCCG 2788
Qy 839 spTTPAspTTPArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuC 859
Db 2789 ACTGGGACTGGAGACACGGCTGCATCCCTTCGCAAGATATGGAGTTATTTGCTGTCTCT 2848
Qy 859 ySileGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTTP 879
Db 2849 GCATAGAAACAAAGCCACTATGTTGCTTTTGTGAAGATATGGGAAGGACGATTTGCTGGC 2908
Qy 879 euPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnV 899
Db 2909 TCTTCTTTGACAGCATGGCCGATCGGATGTGTGTGTCAGATGGCTTTCAACATTTCTCAAG 2968
Qy 899 alThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerL 919
Db 2969 TCACCCCATGCCAGAAAGTAGGAGTACTTTGAAGATGTCTCTGGAAGACCTGCAATTCCT 3028
Qy 919 euAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysM 939
Db 3029 TGGACTCCAGAGAAATCAAGGCTGTGCACGAAGACTGCTTTGTGATGATATATGTGCA 3088
Qy 939 etTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3089 TGTACCAGAGTCCAAACAATGAGTTGTACAAA 3120
RESULT 32
US-09-629-469A-18842
; Sequence 18842, Application US/09629469A
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/09/629,469A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18842
; LENGTH: 2845
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (452)..(2644)
US-09-629-469A-18842
Alignment Scores:

Pred. No.: 0 Length: 2845
Score: 4601.00 Matches: 875
Percent Similarity: 99.32% Conservative: 0
Best Local Similarity: 99.32% Mismatches: 2
Query Match: 91.40% Indels: 4
DB: 28 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-629-469A-18842 (1-2845)

QY 73 LysileuGluGlnProHisAlaValLeuPheValAspGlu---AspValValGluIle 91
DB 2 AAAATCTAGAGCAACCTCATGCAGTCTCTTTGTTGATGAAGAAGATGTTGTAGAGATA 61

QY 92 AsnGluLysPheThrGluLeuLeuAlaIleThrAsnCysGluGluAArgPheSerLeu 111
DB 62 AATGAAAGTTCACAGAGTTACTTTTGGCAATTACCAATTTGTGAGAGAGGTTTCAGCCTG 121

QY 112 PheLysAsnArgAsnArgLeuSerLysGlyLeuGlnIleAspValGlyCysProValLys 131
DB 122 TTTTAAACAAAGAACAGACTAAGTAAGGGCTCCAAATAGACGTGGGCTGTCTGTGAAA 181

QY 132 ValGlnLeuArgSerGlyGluGluLysPheProGlyValValArgPheArgGlyProLeu 151
DB 182 GTACAGCTGAGATCTGGGGAAGAAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTG 241

QY 152 LeuAlaGluArgThrValSerGlyIlePhePheGlyValGluLeuLeuGluGlyArg 171
DB 242 TTAGCAGAGAGGACAGTCTCCGGAATATTTCTTGGAGTTGAAATGCTGGAAGAAGGTCGT 301

QY 172 GlyGlnGlyPheThrAspGlyValTyrglnGlyLysGlnLeuPheGlnCysAspGluAsp 191
DB 302 GGTCAAGGTTTCATCTACGCGGGTGTACCAAGGGAACAGCTTTTTCAGTGTGATGAAGAT 361

QY 192 CysGly---PheValAlaLeuAspLysLeuGluLeuIleGluAspAspAspThrAlaLeu 210
DB 362 TGTGGCGTGTGTGTCATTGGCAAGCTAGACTAGAACTCATGAAGATGATGACACTGCAATG 421

QY 211 GluSerAspTyrrAlaGlyProGlyAspThrMetGlnValGluLeuProProLeuGluIle 230
DB 422 GAAAGTGATTACGCAGTCTCTGGGACACACATGCAGTCAACTCTCTCTTTGGAAATA 481

QY 231 AsnSerArgValSerLeuLysGlyGluThrIleGluSerGlyThrValIlePheCys 250
DB 482 AACTCCAGAGTTCTTTTGAAGTGTGGAGAAACAATAGAACTCTGGAACAGTTATATCTGT 541

QY 251 AspValLeuProGlyLysGluSerLeuGlyTyrrPheValGlyValAspMetAspAsnPro 270
DB 542 GATGTTTTCAGGAAAGAAAGCTTAGGATAATTTTGTGGTGTGGACATGGATAACCCCT 601

QY 271 IleGlyAsnTrpAspGlyArgPheAspGlyVal---LeuCysSerPheAlaCysValGlu 289
DB 602 ATTGGCAACTGGGATGGAAGATTGATGGATGTCAGCTTTGTAGTTTGGCTGTGTGAA 661

QY 290 SerThrIleLeuLeuHisIleAsnAspIleIleProGluSerValThrGlnGluAArg 309
DB 662 AGTACAAATCTATTGACATCAATGATATCATCCAGAGAGTGTGACGCGAGAAAGAGG 721

QY 310 ProProLysLeuAlaPheMetSerArgGlyValGlyAspLysGlySerSerHisAsn 329
DB 722 CCTCCAAACTTGGCCTTTATGTCAAGAGGTGTTGGGACAAAGGTTTCATCCAGTCATAAT 781

QY 330 LysProLysAlaThrGlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPhe 348
DB 782 AAACCAAGGCTACAGGATCTACTCAGACCCCTGGAAATAGAAACAGATCTGAAATATTT 841

QY 349 TyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrp 368
DB 842 TATACCTTAAATGGGTCTTCTGTGCTCACAACCAATCCAAATCAAAAATACATCG 901

QY 369 TyrIleAspGluValAlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPhe 388
DB 902 TACATTGATGAAGTTGCAGAGACCCCTGCAAAATCTCTTACAGAGATATCTACAGACTTT 961

QY 389 AspArgSerSerProProLeuGlnProProValAsnSerLeuThrThrGluAsnArg 408
DB 962 GACCGTTCTTTACACACACCTCAGCTCTCTCTGTGAATCTCACTGACACCCAGAACAGA 1021

QY 409 PheHisSerLeuProPheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHis 428
DB 1022 TTCCACATCTTTTACCATTCAGTCTCACCAGATGCCAATACCAATGGGAAGTATTGGCCAC 1081

QY 429 SerProLeuSerLeuSerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGln 448
DB 1082 AGTCCACTTCTCTGTCTGAGCCAGCTCTGTAATGGAGAGCTAAACACTGACCCCTCCAA 1141

QY 449 GluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeu 468
DB 1142 GAGAGTCACCCCTTGGGCATGCTCTGGGAACCTCACATGCTCTAGAAAGTGGCTCATTTG 1201

QY 469 AlaGluValLysGluAsnProProPheTyrglyValIleArgTTrpIleGlyGlnProPro 488
DB 1202 GCTGNAAGTTAAGGAAGAACCTCTCTCTATGGGGTAATCCGTGGATCGGTACGCCACA 1261

QY 489 GlyLeuAsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAsp 508
DB 1262 GGACTGAATGAGTGTCTGCTGGACTGGAACCTGGAGATGAGTGTGACAGGCTGTACGAT 1321

QY 509 GlyThrPheArgGlyThrArgTyrrPheThrCysAlaLeuLysLysAlaLeuPheValLys 528
DB 1322 GGAACCTTCAGAGCACTCGGTATTTCACTGTCTGCTGAAAGAGGCTGTGTTGTGAAA 1381

QY 529 LeuLysSerCysArgProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIle 548
DB 1382 CTGAAGAGCTGCAGGCCCTGACTCTAGGTTTGCATCATTTGCAGCGGTTTCCAATCAGAT 1441

QY 549 GluArgCysAsnSerLeuAlaPheGlyGlyTyrrLeuSerGluValValGluGluAsnThr 568
DB 1442 GAGCGCTGTAACTCTTTAGCATTTTGGAGGCTACTTAAAGTGAAGTAGTAGAAGAAATACT 1501

QY 569 ProProLysMetGluLysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGln 588
DB 1502 CCACCAAAATGGAAGAAAGGCTTCGAGATATATGATTTGGGAAGAGAAAGGCATCCAG 1561

QY 589 GlyHisTyrrAsnSerCysTyrrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSer 608
DB 1562 GGTCAATTACAAATCTTGTACTTAGACTCAACCTTATTTCTGCTTATTTGCTTTTAGTTCT 1621

QY 609 ValLeuAspThrValLeuLeuAArgProLysGluLysAsnAspValGluTyrrSerGlu 628
DB 1622 GTTCTGGACACTGTGTACTTGGACCCCAAGAAAGAACCGATGTAGATAATATTATAGTAA 1681

QY 629 ThrGlnGluLeuLeuArgThrGluIleValAsnProLeuArgIleTyrrGlyTyrrValCys 648
DB 1682 ACCCAAGAGCTACTGAGGACAGAAATTTGTAATCTCTGAGAAATATATGATATGTGTGT 1741

QY 649 AlaThrLysIleMetLysLeuAArgLysIleLeuGluLysValGluAlaAlaSerGlyPhe 668
DB 1742 GCCACAAAAATTTATGAACCTGAGCAAAATCTTGAAAGGTTGGAGGCTGCATCAGGATTT 1801

QY 669 ThrSerGluLysAspProGluGluPheLeuAsnIleLeuPheHisIleLeuArg 688
DB 1802 ACCTCTGAAGAAAGATCTCTGAGGAATCTTGAATATTTCTGTTTCATCATATTTTAAAG 1861

QY 689 ValGluProLeuLeuLysIleArgSerAlaGlyGlnLysValGlnAspCysTyrrPheTyrr 708
DB 1862 GTAGAACCTTTGCTTAAATAATAGATCAGCAGGTCAAAAGGTTACAAAGATTGTTACTTCTAT 1921

QY 709 GlnIlePheMetGluLysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGlu 728
DB 1922 CAAATTTTATGAAAAAATGAGAAAGTTGGCGTTCACCAATTCAGCAGTGTGTAGAA 1981

QY 729 TrpSerPheIleAsnSerAsnLeuLysPheAlaGluAlaProSerCysLeuIleGln 748
DB 1982 TGGTCTTTTATCAACAGTAACTGAAATTTGACAGGCAACCATCATCTCTGATTATTTCAG 2041

QY 749 MetProArgPheGlyLysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeu 768

Db 2042 ATCCCTCGATTGGAAAGACTTTAAACTATTTAAAAAATTTTCTCTCTCGAATTA 2101
Qy 769 AsnIleThrAspLeuLeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAla 788
Db 2102 AATATAACAGATTACTTGAAGACACTCCACAGACAGTCCCGATATGTGAGGGCTTGCA 2161
Qy 789 MetTyrGluCysArgGluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGln 808
Db 2162 ATGTATGAGTGTAGAGAACTGACGACATCCGACATCTCAGCTGGAATAATCAACGAG 2221
Qy 809 PheCysLysThrCysAsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyr 828
Db 2222 TTTTGTAAAACTGCAACACTCAAGTCCACTTTCATCCGAAGAGGCTGGAATCAATAT 2281
Qy 829 AsnProValSerLeuProLysAspLeuProAspThrAspTrpArgHisGlyCysIlePro 848
Db 2282 AACCCAGTGTCACTTCCAAAGACTTACCCGACTGGGACTGGAGACACGGCTGCATCCCT 2341
Qy 849 CysGlnAsnMetGluLeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPhe 868
Db 2342 TGCAGATATGAGTATTTGCTGTTCTCTGCATAGAAACAGCCACTATGTGCTTTT 2401
Qy 869 ValLysTyrGlyLysAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAsp 888
Db 2402 GTCAAGTATCGGAAGGACGATTTGCTGCTCTTCTTGCACAGCATGGCGCATCGGAT 2461
Qy 889 GlyGlyGlnAsnGlyPheAsnIleProGlnValThrProCysProGluValGlyLysTyr 908
Db 2462 GGTGGTCAAGTATGCTTCAACATTCCTCAAGTCAACCCATGCCAGAAAGTAGGAGATC 2521
Qy 909 LeuLysMetSerLeuGluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAla 928
Db 2522 TTGAGATGCTCTGGAGACCTGCATCTCTTGGACTCCAGGAGATCCAGGCTGTGCA 2581
Qy 929 ArgArgLeuLeuCysAspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyr 948
Db 2582 CGAAGACTGCTTTGTGATGATATATGTGATGTACAGAGTCCCAACATGATGTTGATC 2641
Qy 949 Lys 949
Db 2642 AAA 2644

RESULT 33
US-10-917-503-18842
; Sequence 18842, Application US/10917503
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899

; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18842
; LENGTH: 2845
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (452)..(2644)
US-10-917-503-18842

Alignment Scores:
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Score: 4601.00 Matches: 875
Percent Similarity: 99.32% Conservative: 0
Best Local Similarity: 99.32% Mismatches: 2
Query Match: 91.40% Indels: 4
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US-09-671-687A-3 (1-949) x US-10-917-503-18842 (1-2845)

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Db 2 AAAATTTAGAGCAACCTCATGCAGTTCCTTTGTGATGAAAGGATGTTGTAGAGATA 61
Qy 92 AsnGluLysPheThrGluLeuLeuAlaIleThrAsnCysGluGluArgPheSerLeu 111
Db 62 AATGAAAGTTACAGAGTTACTTTTGGCAATTACCAATTGTGAGGAGAGGTTTCAGCCTG 121
Qy 112 PheLysAsnArgAsnArgLeuSerLysGlyLeuGlnIleAspValGlyCysProValLys 131
Db 122 TTTAAAAACAGAAACAGACTAAGTAAAGGCCCTCCAAATAGACGTGGGCTGTCTGTGAAA 181
Qy 132 ValGlnLeuArgSerGlyGluLysPheProGlyValValArgPheArgGlyProLeu 151
Db 182 GTACAGCTGAGATCTGGGGAAGAAAAATTTCTCTGGAGTTGACGCTTCAGAGGACCCCTG 241
Qy 152 LeuAlaGluArgThrValSerGlyIlePhePheGlyValGluLeuLeuGluGlyArg 171
Db 242 TTAGCAGAGGACAGCTCTCCGGAATATTTCTTGGAGTTGAATGCTGGAAGAGAGTGGT 301
Qy 172 GlyGlnGlyPheThrAspGlyValTyrGlnGlyLysGlnLeuPheGlnCysAspGluAsp 191
Db 302 GGTCAAGGTTTCACTGACGGGGTGTACCAAGGGAAACACAGCTTTTTCAGTGTGATGAAG 361
Qy 192 CysGly---PheValAlaLeuAspLysLeuLeuIleGluAspAspThrAlaLeu 210
Db 362 TGTGGCGTGTGTTGTTGCAATTTGGACAAGCTAGAACTCATAGAAAGATGATGACACTGATG 421
Qy 211 GluSerAspTyrAlaGlyProGlyAspThrMetGlnValGluLeuProLeuGluIle 230
Db 422 GAAAGTGATTACGAGGCTCTGGGGGACACAATGACAGGTCGAACCTTCTCTTTGGAATA 481
Qy 231 AsnSerArgValSerLeuLysGlyGlyThrIleGluSerGlyThrValIlePheCys 250
Db 482 AACTCCAGAGTTTCTTTGAAGGTTGGAGAAACAATAGAACTCTGGAACAGTATATCTGT 541
Qy 251 AspValLeuProGlyLysGluSerLeuGlyTyrPheValGlyValAspMetAspAsnPro 270
Db 542 GATGTTTTCAGGAGAAAGAGCTTAGGATATTTGTTGGTGTGGACATGATGAACCT 601
Qy 271 IleGlyAsnTrpAspGlyArgPheAspGlyVal---LeuCysSerPheAlaCysValGlu 289
Db 602 ATTCGCAACTGGGATGGAAGATTTGATGGAGTGCAGCTTTGTAGTTTTCGGGTGTGTA 661
Qy 290 SerThrIleLeuLeuHisIleAsnAspIleIleProGluSerValThrGlnGluArgArg 309
Db 662 AGTACAATTCTATTGCAATCATGATATCATCCAGAGAGTGTGACGAGGAGGAGG 721

QY 310 ProProLysLeuAlaPheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsn 329
Db 722 CTTCCCAAACTTGGCTTTATGTCAGAGAGGTGTGGGACAAAGGTTTCATCCAGTCATAAT 781
QY 330 LysProLysAlaThrGlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPhe 348
Db 782 AACCAAGGCTACAGGATCTACCTCAGACCTCGAATAAGAACAGATCTGAATATTATTT 841
QY 349 TyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrp 368
Db 842 TATACCTTAAATGGGTCTTCTGTGACTCAACACCAATCCAAATCAAAAAATACATGG 901
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Db 902 TACATTGATGAAGTGCAGAGACCTCGCAAAATCTCTTACAGAGATATCTACAGACTTT 961
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Db 1022 TTCACCTCTTACCATTCAGTCTCACCAAGATGCCAATACCAATGAAGTATTGGCCAC 1081
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Db 1082 AGTCCACTTTCTCTGTGAGCCAGTCTGTAAATGAAGAGCTAAACACTGCACCCGTCCAA 1141
QY 449 GluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeu 468
Db 1142 GAGAGTCCACCTTGGCCATGCTCTGCGAAGTCAACATGGTCTAGAAGTGGGCTCATTTG 1201
QY 469 AlaGluValLysGluAsnProProPheTyrGlyValIleArgTTPilIleGlyGlnProPro 488
Db 1202 GCTGAAGTTAAGAGAACCTCTCTTCTATGGGGTAATCCGTTGGATCGGTACGCCACA 1261
QY 489 GlyLeuAsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAsp 508
Db 1262 GGACTGAATGAAGTCTGCTGGACTGGAATCGAGTGTGCGAGCTGTACGGAT 1321
QY 509 GlyThrPheArgGlyThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLys 528
Db 1322 GGAACCTTCAGAGGCATCTGGTATTTTCCCTGTGCTGCCCTGAAGAAGGCGCTGTTGTGAAA 1381
QY 529 LeuLysSerCysArgProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIle 548
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QY 549 GluArgCysAsnSerLeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThr 568
Db 1442 GAGCGTGTAACTCTTTAGCATTTGGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACT 1501
QY 569 ProProLysMetGluLysGluGlyLeuGluIleMetIleGlyLysLysGlyIleGln 588
Db 1502 CCACCAAAAAATGAAAAAAGGCTTGGAGATAATGATTGGGAAGAAAGGATCCAG 1561
QY 589 GlyHisTyrAsnSerCysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSer 608
Db 1562 GGTCAATTACAAATTTGTTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTAGTTCT 1621
QY 609 ValLeuAspThrValLeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGlu 628
Db 1622 GTTCTGGACACTGTGTACTTTGACCAACCAAGAAAGAACGATGTAGAAATATTATAGTGA 1681
QY 629 ThrGlnGluLeuLeuArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCys 648
Db 1682 ACCCAAGAGCTACTGAGGACAGAAATGTTAACTCTGAGATATATGATATGTGTGT 1741
QY 649 AlaThrLysIleMetLysLeuArgLysIleLeuGluLysValGluAlaAlaSerGlyPhe 668
Db 1742 GCCACAAAAATATTGAAACTGAGGAAAAATCTTTGAAAAAGGTGAGGCTGCATCAGGATTT 1801

QY 669 ThrSerGluGluLysAspProGluGluPheLeuAsnIleLeuPheHisIleLeuArg 688
Db 1802 ACCTCTGAAGAAAAAGATCCTGAGGAATTTCTTGAATATTCTCTTTTCATCATATTTTAAAG 1861
QY 689 ValGluProLeuLeuLysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyr 708
Db 1862 GTAGAACCTTTGCTTAAATAAATAGATCAGCAGGTCAAAAGGTCAAGATTGTTACTTCTAT 1921
QY 709 GlnIlePheMetGluLysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGlu 728
Db 1922 CAAATTTTATGAAAAAAATGAGAAAGTGTGGCGTTCACCAATTCAGCAGTTGTTAGAA 1981
QY 729 TrpSerPheIleAsnSerAsnLeuLysPheAlaGluAlaProSerCysLeuIleGln 748
Db 1982 TGGTCTTTTATCAACAGTAACCTGAAATTTGCAGAGGCACCATCATCTGTGATTATTCAG 2041
QY 749 MetProArgPheGlyLysAspPheLysLeuPheLysIlePheProSerLeuGluLeu 768
Db 2042 ATGCTCTGATTGGAAAGACTTTTAAACTATTAAAAAAATTTTCTCTCTGGAATTA 2101
QY 769 AsnIleThrAspLeuLeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAla 788
Db 2102 AATATAACAGATTACTTTGAAGACACTCCAGACAGTGTCCGGATATGTGGAGGCTTGA 2161
QY 789 MetTyrGluCysArgGluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGln 808
Db 2162 ATGTATGAGTGTAGAGAAATGCTACGACGATCCGACATCTCAGCTGGAATAATCAAGCAG 2221
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Db 2222 TTTTGTAAAACTCCAACTCAAGTCCACTTTCATCCGAAGAGGCTGAATCATAAATAT 2281
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Db 2282 AACCCAGTGTCACTTCCAAAGACTTACCCGACTGGGACTGGAGACAGGCTGCATCCCT 2341
QY 849 CysGlnAsnMetGluLeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPhe 868
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QY 869 ValLysTyrGlyLysAspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAsp 888
Db 2402 GTGAAGTATGGGAAGGACGATTTCCCTGGCTCTTCTTTGACAGCATGCCGATCGGAT 2461
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Db 2462 GGTGGTCAAGATGGCTTCAACATTTCTCAAGTCCACCCATGCCAGAAAGTAGGAGATAC 2521
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Db 2522 TTGAAGATGCTCTGGGAAGACCTGCATTTCTTGGACTCCAGAGAAATCCAGGCTGTGA 2581
QY 929 ArgArgLeuLeuCysAspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyr 948
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QY 949 Lys 949
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Search completed: January 16, 2006, 14:11:35

Job time : 10028 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 23:07:39 ; Search time 992 Seconds
(without alignments)
1433.440 Million cell updates/sec

Title: US-09-671-687A-3
Perfect score: 5034
Sequence: 1 MSSGLMSQEKVTSYWEERI.....RLICDAYMCVQSFTMSLYK 949

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3169381 seqs, 749195308 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=rlp
-Q=/cgn2_1/USPTO_spool_p/US09671687/runat_13012006_114914_2482/app_query.fasta_1.1095
-DB=Pending_Patents_NA_New -QFMT=fastcap -SUFFIX=90pct.rnnp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=500 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=90 -ALIGN=500 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000
-USER=US09671687@cgn_1_1_10@runat_13012006_114914_2482 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
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7: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq1:*
9: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Query Match	Length DB ID	Description
1	4983	99.0 3540	9 US-11-266-748A-25871 Sequence 25871, A
2	4971.5	98.8 5371	10 US-60-751-420-3015 Sequence 3015, Ap

ALIGNMENTS

RESULT 1

US-11-266-748A-25871
; Sequence 25871, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55915-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25871
; LENGTH: 3540
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25871

Alignment Scores:
Pred. No.: 0 Length: 3540
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 99.99% Indels: 4
DB: 9 Gaps: 4

US-09-671-687A-3 (1-949) x US-11-266-748A-25871 (1-3540)

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Db	277	ATGAGTTTCAGGCTTATGGAGCAAGAAAAAGTCACTTCACCCCTACTGGGAGAGCGGATT	336
Qy	21	PhetyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys	40
Db	337	TTTTACTTGCTTCTCAAGAAATGCGCGTTACAGCAAAACAAACAAAGCTCTTTAA	396
Qy	41	ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArg	60
Db	397	GTACCGAAGGAAGTATAGGACAGTATATTCAGATCGTTCTGTGGGCAATCAAGATT	456
Qy	61	ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla	80
Db	457	CTTCTCAAAGGCAAGAAAAATCAGATTGATTAAAAATTTAGAGCAACCTCATGCA	516
Qy	81	ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu	99
Db	517	GTTCTCTTGTGATGAAAGAGTGTGTAGAGATAAATGAAAGATTTCACAGATTACTT	576
Qy	100	LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer	119
Db	577	TTGGCAATTACCAATTGTGAGGAGAGGTTACGCCCTGTTTAAAAACAGAAACAGATAAGT	636
Qy	120	LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu	139
Db	637	AAAGCCCTCCAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTCAGATCTGGGGAAGNA	696

QY	140	LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly	159	
Db	697	AAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTAGCAGAGACAGTCTCCGGA	756	
QY	160	IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal	179	
Db	757	ATATTTCTTGGAGTTGAATTTGCTGGAGAGAGGTCGTGGTCAAGGTTTTCACGTACGGGGTG	816	
QY	180	TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp	198	
Db	817	TACCAAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTCATTTGGAC	876	
QY	199	LysLeuGluLeuLeuGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218	
Db	877	AAGCTAAGACTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACGCAGGTCCTGGG	936	
QY	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238	
Db	937	GACACAATGCAGGTCGAACCTCTCTCTTTGGAAATAAACTCCAGAGTTTCTTTGAAGGTT	996	
QY	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258	
Db	997	GGAGAAACAATAGAACTCGGAACAGTTATATTTCTGTGATGTTTGGCAGGAAAGAAAGC	1056	
QY	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTyrAspGlyArgPhe	278	
Db	1057	TTAGGATATTTTGTGTGTGGACATGATGATACCTATTGGCAACTGGGATGGAGATT	1116	
QY	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297	
Db	1117	GATGGAGTCAGCTTTGTAGTTTTCGTGTTGTGAAAGTAGTCAATTTCTATTGCACATCAAT	1176	
QY	298	AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer	317	
Db	1177	GATATCATCCAGAGAGTGTGACGACGAGAGGAGGCTCCCAACTTGCCTTTATGTCA	1236	
QY	318	ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr	337	
Db	1237	AGAGGTGTGGGACAAAGGTTCTATCCAGTCATATTAACCAAGGCTACAGGATCTACC	1296	
QY	338	SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal	356	
Db	1297	TCAGACCTCGGAAATAGAAACAGATCTGAAATTTATTTATACCTTAAATGGGTCTCTGTT	1356	
QY	357	AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp	376	
Db	1357	GACTCAACACCAATCCAAATCAAAATACATGATGATGATGATGATGATGATGATGATGAT	1416	
QY	377	ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln	396	
Db	1417	CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGCTTCTTCCACCACTCCAG	1476	
QY	397	ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu	416	
Db	1477	CCTCCTCTGTGAATCACTGACACCGAGACAGATTCCACTCTTTACCATTCAGTCTC	1536	
QY	417	ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln	436	
Db	1537	ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGTCAGCCGAG	1596	
QY	437	SerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro	456	
Db	1597	TCTGTAAATGGAAGAGCTTAAACACTGCAACCCGTCACAGAGAGTCCACCTTTGGCCATGCC	1656	
QY	457	ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro	476	
Db	1657	CCTGGGAACTCATATGTCTAGAGTGGGCTCATTTGGCTGAGTTAGGAGAACCTTCTCT	1716	
QY	477	PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly	496	
Db	1717	TTCTATGGGTAAATCCGTGGATCGGTGAGCCAGCCAGGACTGAATGAAGTGTCTCGCTGGA	1776	
QY	497	LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgTyr	516	
Db	1777	CTGGAACCTGGAAGATGATGTGCAAGGCTGTACCGATGTAACCTTCAGAGGCACTCGTAT	1836	
QY	517	PheThrCysAlaLeuLeuValLeuAlaLeuPheValLysLeuLysSerCysArgProAspSer	536	
Db	1837	TTCACTGTGCCCCTGAAGAAGGCGCTGTGTGTGAAACTGAAGAGCTGCAGGCGCTGACTCT	1896	
QY	537	ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe	556	
Db	1897	AGGTTTGCATCATTCAGCCGGTTTCCATTCAGATTGAGCGCTGTAACTCTTTAGCAITTT	1956	
QY	557	GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly	576	
Db	1957	GGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAGAAAGAGC	2016	
QY	577	LeuGluIleMetIleGlyLysLeuLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu	596	
Db	2017	TTGAGAGATAATGATTTGGGAAGAAAGAGGCTACAGGCTCATTAACATTTCTTTACTTTA	2076	
QY	597	AspSerThrLeuPheCysLeuPheAlaPheSerValLeuAspThrValLeuLeuArg	616	
Db	2077	GACTCAACCTTATTTCTGCTTATTTGCTTTTAACTTCTGTTCTGGACACTGTGTACTTAGA	2136	
QY	617	ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu	636	
Db	2137	CCCAAGAAAGAAACGATGTAGAATATTTATAGTGAACCCCAAGAGCTACTGAGGACAGAA	2196	
QY	637	IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg	656	
Db	2197	ATTGTTTAACTCTCTGAGAAATATATGAGATGTGTGTGCCACAAATATTTGAAACTGAGG	2256	
QY	657	LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu	676	
Db	2257	AAATATCTTGAAGAGGTGGAGCTGCATCAGATTTTACTCTGAAGAAAGATCTCTGAG	2316	
QY	677	GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg	696	
Db	2317	GAATTTCTTGAATATTTCTGTTTTCATATATTTTAAAGGTAGAACCTTTGCTAAAAATAAGA	2376	
QY	697	SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu	716	
Db	2377	TCAGCAGGTCAAAAGGTACAGATTTGTTACTTCTATCAAAATTTTATGAAAAAATGAG	2436	
QY	717	LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu	736	
Db	2437	AAAGTTGGCGTTCACCAATTCAGAGTGTGTAGATGTGTCTTTTATCAACAGTAACTCTG	2496	
QY	737	LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe	756	
Db	2497	AAATTTGCAGAGGACCATCATGTTCTGATTTATTCAGATGCTCGATTTGGAAAAAGACTTT	2556	
QY	757	LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp	776	
Db	2557	AAACTATTTAAAAAATTTTCTCTCTGAAATTAATATAACAGATTTTACTTGAAGAC	2616	
QY	777	ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr	796	
Db	2617	ACTCCACAGACAGTCCCGATATGTGGAGGCTTGCATGTATGATGATGATGATGATGATGAT	2676	
QY	797	AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln	816	
Db	2677	GACGATCCGGACATCTCAGCTGGAAAAAATCAAGCAGTGTGTGTAACCTGCAACTCAA	2736	
QY	817	ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp	836	
Db	2737	GTCCACCTTTCATCCGAGAGGCTGAATCATATAATAACCCAGTGTCACTTCCCAAGAC	2796	
QY	837	LeuProAspThrAspThrArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla	856	
Db	2797	TTATCCGACCTGGGACTGGAGACACGGCTGCACTCCCTTCCAGAAATATGGAGTTATTTGCT	2856	
QY	857	ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer	876	

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Db 2857 GTTCTCTGCATAGAAACAACCCACTATGTGTCTTTTGTGAGATATGGGAAGGACGATTCT 2916
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2917 GCCTGGCTCTTCTTTCACAGCATGGCCGATCGGATGGTGGTTCAGAAATGSCITTCACATT 2976
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2977 CTTCAAGTCACCCCATGCCAGAAAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTG 3036
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 3037 CATTCCTTGGACTCCAGAGAAATCCAGGCTGTGCAGAGACTGCTTTGTGATGCATAT 3096
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3097 ATGTGCATGTACCAGAGTCCAAACAATGAGTTTGTACAAA 3135

RESULT 2
US-60-751-420-3015
; Sequence 3015, Application US/60751420
; GENERAL INFORMATION:
; APPLICANT: Raelson, John Verner
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Bradley, Walter Edward
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Debrus, Sophie
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Little, Randall David
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: GeneMap of the human genes associated with Crohn's disease
; FILE REFERENCE: GENT-011/00US
; CURRENT APPLICATION NUMBER: US/60/751,420
; CURRENT FILING DATE: 2005-12-19
; NUMBER OF SEQ ID NOS: 27266
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3015
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homosapiens
US-60-751-420-3015

Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 10 Gaps: 5

US-09-671-687A-3 (1-949) x US-60-751-420-3015 (1-5371)

QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 392 ATGAGTTTCAGGCTTATGAGCCCAAGAAAAAGTCACTTCACCCCTACTGCGGAAGCGGATT 451
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 452 TTTTACTTGTCTTCAAGAAATGCAGCTTACAGACAAACAAACAAACAAAGCTCTTAA 511
QY 41 ValProLysGlySerIleGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 512 GTACCAAGGGAAGATATAGACAGTATATTCAGATCGTTCGTGTGGGGCATTTCAAGATT 571
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
Db 572 CCTTCTGCAAAAGGCAAGAAAATCAGATTGGATTAAATAATTCAGACCACTCATGCA 631
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QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 632 GTTCTCTTCTTGTATGAAAAAGGATGTTCTGAGATAAAATGAAAAATTCACAGAGTTACTT 691
QY 100 LeuAlaIleThrAsnCysGluGluAtrgPheSerLeuPheLysAsnAtrgAsnArgLeuSer 119
Db 692 TTGGCAATTACCAATTGTGAGGAGAGGTTCAGCCTGTTTAAAAACAGAAAACAGACTAAGT 751
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuAtrgSerGlyGluGlu 139
Db 752 AAAGGCTCCAAATAGACGTGGGCTGTCCTGTGAAAGTACAGCTGAGATCTGGGGGAAGA 811
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluAtrgThrValSerGly 159
Db 812 AAAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGA 871
QY 160 IlePhePheGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 872 ATATTTCTTGGAGTTGAAATTGCTGGAAGAAGGTGCTGTCGTCAGAGTTTTCACAGCGGGTG 931
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 932 TACCAAGGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTGTCATTGGAC 991
QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 992 AAGCTAGAACTCATAGAAGATGATGACACTGCACTTGGAAGTGTATTCGCGAGGCTCTGGG 1051
QY 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 1052 GACACAATGCAAGTTCGAACCTCTCTTTGGAATAAATCCAGAGTTTCTTTCGAAGTT 1111
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 1112 GGAGAAACAATAGAACTGGAACAGTTATATCTGTCATGTTGTTGCCAGGAAAAAGAAC 1171
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1172 TTAGGATATTTGTTGGTGGACATGGATAACCTATTTGGCAACTGGGATGGGAAGATT 1231
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1232 GATGGAGTGCAGCTTTGTTAGTTTGGCTGTGTGAAAGTACAAATCTTATTGCACATCAAT 1291
QY 298 AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314
Db 1292 GATATCATCCAGCTTTATCAGAGAGTGTGACGAGGAAAGGAGGCGCTCCCAAACTTGCC 1351
QY 315 PheMetSerArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThr 334
Db 1352 TTTTATGTCAAGAGTGTGGGGACAAAGTTTCATCCAGTCATATAATAAACCAAGGCTTACA 1411
QY 335 GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly 353
Db 1412 GGATCTACCTCAGACCTCGGAAATAGAAACAGATCTCGAATATTTATTTTATACCTTAATGGG 1471
QY 354 SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTyrTyrIleAspGluVal 373
Db 1472 TCTTCTGTTGACTCACAACCAATCCAAATCAAAAATACAAATACATGTTGATGAAAGTT 1531
QY 374 AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerPro 393
Db 1532 GCAGAAAGACCTTCGCAAAATCTTTACAGAGATATCTACAGACTTTTGACCGTCTTCACCA 1591
QY 394 ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413
Db 1592 CCACTCCAGCTCTCTCTGTGAATCTACTGACCAACCGAGAACAGATTTCCACTCTTACCA 1651
QY 414 PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433
Db 1652 TTCAGTCTCACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTG 1711
QY 434 SerAlaGlnSerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProLeu 453
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Db 1712 TCAGCCAGCTCTGTAATGGAAGACTAAACACTGSCACCCGCTCCAAAGAGAGTCCACCCCTTG 1771
Qy 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473
Db 1772 GCCATCCCTCCTGGGAACCTCACATGGTCTAGAAAGTGGGCTCATTTGGCTGAAGTTTAGGAG 1831
Qy 474 AsnProProPheTyrGlyValIleAArgTTPilGlyGlnProProGlyLeuAsnGluVal 493
Db 1832 AACCCCTCCTTCTATGGGTAAATCCGTGGATCGGTGAGCCACAGGACTGAATGAAGTG 1891
Qy 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513
Db 1892 CTGCTGGGACTGGAACCTGGAAGATGAGTGTGAGGCTGTACGGATGGAACTTCAGAGGC 1951
Qy 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArg 533
Db 1952 ACTCGGTATTTACCTGTGCCCCGGAAGAGGCGCTGTTGTGAACCTGAAGAGCTGCAGG 2011
Qy 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553
Db 2012 CCTGACTCTAGGTTTGATCATTTGACCGCGTTCATCATCAGATTGAGCGCTGTAACTCT 2071
Qy 554 LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573
Db 2072 TTAGCAATTTGGAGGCTACTTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAA 2131
Qy 574 LysGluGlyLeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSer 593
Db 2132 AAAGAAGGCTTGAGATAATGATTTGGGAAGAAAGGCAATCCAGGCTCATTAACAATTC 2191
Qy 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAsnThrVal 613
Db 2192 TGTACTTAGACTCAACCTTATTTCTGCTATTTGCTTTTGTAGTTCTGTCTGGACACTGTG 2251
Qy 614 LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633
Db 2252 TTACTTAGACCCAAAGAAAGACGATGTAGATAATATTATAGTGAACCCCAAGAGCTACTG 2311
Qy 634 ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653
Db 2312 AGGACAGAAATTTGTAATCCTCTGAGAAATATATGAGATATGTGTGTCACCAAAATTTATG 2371
Qy 654 LysLeuArgLysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLys 673
Db 2372 AAATGAGGAAATATCTGAAAAGGTGGAGGCTGCATCAGGATTTACTCTATCAAAATTTTATG 2431
Qy 674 AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693
Db 2432 GATCCTGAGGAATCTTGAATATTTCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTA 2491
Qy 694 LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713
Db 2492 AAAATAAGATCAGCAGGTCAAAAGGTACAGATTTGTTACTTCTATCAAAATTTTATG 2551
Qy 714 LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluThrPheIleAsn 733
Db 2552 AAAAATGAGAAAGTTGGCGTTCCCAAAATTCAGCAGTTGTTAGAAATGGTCTTTTATCAAC 2611
Qy 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753
Db 2612 AGTAACCTGAAATTTGAGAGGACCATCATGCTGATTAATTCAGATGCGCTCGAATTTGGA 2671
Qy 754 LysAspPheLysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
Db 2672 AAAGACTTTTAAACTATTTTAAAAATTTTCTTCTCTGGAATTTAAATATAACAGATTTA 2731
Qy 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
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Qy 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
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Qy 834 ProLysAspLeuProAspTyrAspTyrPArgHisGlyCysIleProCysGlnAsnMetGlu 853
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Qy 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
Db 2972 TTATTTGCTGTTCTCTCATAGAAACCAAGCCACTATGTTGCTTTGTGAAGTATGGGAG 3031
Qy 874 AspAspSerAlaTyrLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893
Db 3032 GACGATTTCCCTGGCTCTTCTTTGACAGCATGTCGCCGATCGGATGGTGGTCAGANTGGC 3091
Qy 894 PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913
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Qy 914 GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys 933
Db 3152 GAAGACCTGCATTCCTTTGGACTCCAGGAGAAATCCAAAGCTGTGCACGAAAGACTGCTTTGT 3211
Qy 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
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Search completed: January 16, 2006, 14:23:54

Job time : 1011 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 21:47:59 ; Search time 42759 Seconds
(without alignments)
1261.593 Million cell updates/sec

Title: US-09-671-687A-3
Perfect score: 5034
Sequence: 1 MSGLWSQEKVTSFYWEERI.....RLLCDAYMCMYQSPMSLYK 949

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09671687/runat_13012006_114913_2460/app_query.fasta.1.1095
-DB=GenBank -QFMT=fastap -SUFFIX=90pct.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=90 -ALIGN=500 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09671687 @CGN 1.1 5931 @runat_13012006_114913_2460 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBank 149:*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sy.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4983	99.0	3302	6	CQ834224 Sequence
2	4983	99.0	3540	8	BC012342 Homo sapi
3	4983	99.0	5414	6	CS034166 Sequence

4	4983	99.0	5414	6	CS043118 Sequence
5	4983	99.0	5414	8	AB020656 Homo sapi
6	4980	98.9	3302	6	CQ834222 Sequence
7	4971.5	98.8	5371	8	H9A250014 Homo sapi
8	4968.5	98.7	3311	6	CQ834226 Sequence
9	4962	98.6	3480	6	CQ719792 Sequence
10	4942	98.2	4527	6	BD231207 Human cyt
11	4718.5	93.7	4314	9	AK122389 Mus muscu
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ALIGNMENTS

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DEFINITION Sequence 95 from Patent WO2004058805.
ACCESSION CQ834224
VERSION CQ834224.1 GI:50833761
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
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AUTHORS Matsuda, A. and Yoneta, S.
TITLE T cell activating gene
JOURNAL Patent: WO 2004058805-A 95 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
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ORIGIN

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AUTHORS			
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		Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,	
		Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,	
		Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,	
		Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,	
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		Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,	
		McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,	
		Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,	

TITLE	
JOURNAL	Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
PUBMED	Fahey,J., Helton,E., Kettner,M., Madan,A., Rodrigues,S.,
REFERENCE	Sanchez,A., Whiting,M., Madan,A.C., Young,A.C., Shevchenko,Y.,
AUTHORS	Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
TITLE	Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
JOURNAL	Butterfield,Y.S., Krzywinski,W.I., Skalska,U., Smallus,D.E.,
	Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
	Generation and initial analysis of more than 15,000 full-length
	human and mouse cDNA sequences
	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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	Strausberg,R.
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	Submitted (15-AUG-2001) National Institutes of Health, Mammalian
	Gene Collection (MGC), Cancer Genomics Office, National Cancer
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
	USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk
	Email: cgapbs-r@mail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Rubin Laboratory
	DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
	BC Cancer Agency, Vancouver, BC, Canada
	info@bcgsc.bc.ca
	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
	Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
	Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
	Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
	Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
	Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
	Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
	George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES	
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misc feature

misc feature

ORIGIN

Alignment Scores:

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US-09-671-687A-3 (1-949) x BC012342 (1-3540)

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VERSION CS034166.1 GI:60732866
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REFERENCE
1 Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.
AUTHORS Compositions and methods for the treatment of immune related
TITLE diseases
JOURNAL Patent: WO 2005016962-A 3672 24-FEB-2005;
Genentech, Inc. (US)
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 VERSION CS043118.1 GI:61850143
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 Homnidae; Homo.
 REFERENCE 1
 AUTHORS Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I. and Wu, T. D.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005019258-A 3672 03-MAR-2005;
 Genentech, Inc. (US)
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LOCUS Homo sapiens mRNA for KIAA0849 protein, partial cds.
DEFINITION AB020656
ACCESSION AB020656
VERSION AB020656.2 GI:14133220
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 5414)
AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hiroseawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
JOURNAL DNA Res. 5 (6), 355-364 (1998)
PUBMED 10048485
REFERENCE 2 (bases 1 to 5414)
AUTHORS Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
COMMENT On May 17, 2001 this sequence version replaced gi:4240186.
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ORIGIN

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US-09-671-687A-3 (1-949) x AB020656 (1-5414)

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CQ834222

LOCUS CQ834222 3302 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 93 from Patent WO2004058805.
ACCESSION CQ834222
VERSION CQ834222.1 GI:50833759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Matsuda, A. and Yoneta, S.
TITLE T cell activating gene
JOURNAL Patent: WO 2004058805-A 93 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
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ORIGIN

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ACCESSION  AJ250014
VERSION    AJ250014.1 GI:8250235
KEYWORDS   cyld gene; Familial Cyldromatosis.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE
AUTHORS    Bignell,G.R., Brown,C., Biggs,P.J., Lakhani,S.R., Jones,C.,
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            Swift,S., Smith,A., Ashworth,A. and Stratton,M.R.
            Identification of the familial cyldromatosis tumour-suppressor
            gene
JOURNAL    Nat. Genet. 25 (2), 160-165 (2000)
PUBMED     10835629
REFERENCE  2 (bases 1 to 5371)
AUTHORS    Stratton,M.R.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-1999) Stratton M.R., Cancer Genetics, Institute
            of Cancer Research, 15 Cotswold Rd., Sutton, Surrey, SM2 5NG.,
            UNITED KINGDOM
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ORIGIN
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Best Local Similarity: 99.16%      Mismatches: 1
Query Match:      98.76%      Indels:      7
DB:              8      Gaps:      5

US-09-671-687A-3 (1-949) x HSA250014 (1-5371)

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            Homnidae; Homo.
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AUTHORS    Matsuda,A. and Yoneta,S.
TITLE      T cell activating gene
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US-09-671-687A-3 (1-949) x CQ834226 (1-3311)

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Db 2583 CTTGAAGACACTCCAGACAGTGGCGGATATGTGGAGGCTTGCATATGTATGATGTAGA 2642
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Db 3003 GAAGACTGCTATCTTGGACTCCAGGAGATCCAAAGCTGTGCAGAGACTGCTTTGT 3062
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CQ719792
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DEFINITION Sequence 5726 from Patent WO02068579.
ACCESSION CQ719792
VERSION CQ719792.1 GI:42280649
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 5726 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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Percent Similarity: 99.27% Conservative: 0
Best Local Similarity: 99.27% Mismatches: 2
Query Match: 98.57% Indels: 5
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Db 235 ATGAGTTTCAGGCTTATGAGCCAAAGAAAGTCACTTCACTTCACTGCGAAGAGCGGATT 294

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Db	475	GTCTCTTTGTGTATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCCACAGATTACTT	534	Db	1555	GTCTGTAATGGAAGAGCTAAACACTGCACCCGTCACAGAGAGTCCACCCTTGGCCATGCC	1614
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Qy	160	IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal	179	Qy	516	xPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSe	536
Db	715	ATATTTCTTGGAGTTGAATTCGTGGAAGAGTCTGTGTCGAAGGTTTCACTGACGGGGTG	774	Db	1795	TTTTCACCTGTGCCCTGGAAGAGGCGCTGTTTGTGAAACTGAAGAGCTGCAGGCCCTGACTC	1854
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Db	775	TACCAAGGGAACACAGCTTTTTCAGTGTGTGAAGATTGTGCGCGTGTGTTGTCATTGGAC	834	Db	1855	TAGGTTTGGCATCATTCGACGCGGTTTCCAAATCAGATTGAGCGCTGTAATCTCTTTAGCATT	1914
Qy	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218	Qy	556	eGlyGlyTyrLeuSerGluValValGluAsnThrProProLysMetGluLysGluGlu	576
Db	835	AAGCTAGAACCTCATAGAAGATGATGACACTGCATTGGAAGATGATTACGCACAGTCTCTGGG	894	Db	1915	TGGAGGCTACTTTAAGTAGTAGTAGAAGAAATACTCCACAAAATGGAAGAAAGAGG	1974
Qy	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238	Qy	576	yLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrIle	596
Db	895	GACCAATGACGTCGAACTTCTCTTGTGGAATTAATCTCCAGATTTCCTTTGAGGTT	954	Db	1975	CTTGAGATATATGATTGGGAAGAAAGGCAATCCAGCGTCATTACAATCTTGTACTTT	2034
Qy	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258	Qy	596	uAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuAr	616
Db	955	GGAGAAACAATAGAAATCTGGAACAGTTATATCTGTGATGTTTGGCCAGGAAAGAAAGC	1014	Db	2035	AGACTCAACCTTATCTGCTTATTTGCTTTTGTGTTCTCTCTGGACACTGTGTACTTAG	2094
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Qy	298	AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer	317	Qy	656	gLyIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu	676
Db	1135	GATATCATCCAGAGAGTGTACAGCAGGAAGAGGCGCTCCCAAACTTCGCTTTATGTCA	1194	Db	2215	GAAAATACTTGAAGGTGGAGGCTGCATCAGGATTTTACCTCTGAAGAAAAAGATCCTGA	2274
Qy	318	ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr	337	Qy	676	uGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleAr	696
Db	1195	AGAGTGTGGGCAAAAGTTTCATCCAGTCAATAAACAAGGCTTACAGGATCTACC	1254	Db	2275	GGAATTTCTTGAATATCTGTTTCATCATATTTTAAGGGTAGAACCTTTCTCTAAAAATAAG	2334
Qy	338	SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal	356	Qy	696	gSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu	716
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Qy	357	AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGlu-ValAlaGluAs	376	Qy	716	uLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLe	736
Db	1315	GACTCACACACCAATCCAAATCAAAAATACATGGTACATTGATGAAGGTTGCGAAGA	1374	Db	2395	GAAAGTTGGCGTTCCCACAATTCAGCAGTTGTTGAATGGTCTTTTATCAACAGATAACCT	2454
				Qy	736	uLysPheAlaGluAlaProSerCysLeuIleGlnMetProArgPheGlyLysAspPh	756

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Qy	222	GlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyThr	241	Qy	580	MetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerThr	599
Db	929	CAGGTGGAACCTTCTCTCTTTGGAAATAAATCCAGAGTTTCTTTGAAGGTTGGAGAAACA	988	Db	2009	ATGATTGGGAAGAAGAAGGCATCCAGGTCAATTAACAATTTCTTTACTTTAGACTCAACC	2068
Qy	242	IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr	261	Qy	600	LeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysGlu	619
Db	989	ATAGAACTGGAAACAGTTATATCTGTGATGTTTTGGCAGAAAGAAGCTTAGGATAT	1048	Db	2069	TTATTCCTGTTATTTGCTTTTGTAGTTCTGTCGACACTGTTGTTACTTAGACCAAGAA	2128
Qy	262	PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal	281	Qy	620	LysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValAsn	639
Db	1049	TTTGTGTTGGTGTGGACATGGATAACCTTATTGGCAACTGGGATGGAGATTTGATGGAGTG	1108	Db	2129	AAGAACGATGTAGAATAATTATAGTGAACCCCAAGAGCTACTGAGGACAGAAATTTGTTAA	2188
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Db	1109	CAGCTTTGTAGTTTTGGGTGTGTTGTAAGTACAATTTCTATTGGCACATCAATGATATCATC	1168	Db	2189	CCTCTGAGAATATATGGATATGTGTGTGCCCAAAAATTTATGAAACTGAGGAAAAATACTT	2248
Qy	301	ProGluSerValThrGlnGluArgAtqProProLysIleuAlaPheMetSerArgGlyVal	320	Qy	660	GluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLeu	679
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Qy	360	ProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAspProAlaLys	379	Qy	720	ValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeuLysPheAla	739
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RESULT 11
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ACCESSION AK122389
VERSION GI:28972434
KEYWORDS FLI CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
TITLE Prediction of the coding sequences of mouse homologues of KIAA
gene: II. The complete nucleotide sequences of 400 mouse
KIAA-homologous cDNAs identified by screening of terminal sequences
of cDNA clones randomly sampled from size-fractionated libraries
JOURNAL DNA Res. 10, 35-48 (2003)
AUTHORS Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2003) Hisaishi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-Kamatori, Kisarazu, Chiba 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
COMMENT The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing; Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
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ORIGIN

Alignment Scores:

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US-09-671-687A-3 (1-949) x AK122389 (1-4314)

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BC042438 4501 bp mRNA linear ROD 30-JUN-2004
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DEFINITION Clone MGC:25429 IMAGE:3983771), complete cds.
ACCESSION BC042438
VERSION BC042438.1 GI:27503670
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4501)

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RESULT 13

BC082001

LOCUS

DEFINITION

BC082001 3267 bp mRNA linear ROD 09-MAY-2005
Rattus norvegicus retinitis pigmentosa 1 (autosomal dominant)
(predicted), mRNA (cdna clone MGC:94236 IMAGE:7131198), complete
cds

ACCESSION

BC082001 GI:51858716

VERSION

BC082001.1 Rattus norvegicus (Norway rat)

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 3267)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hele, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE

AUTHORS

NIH MGC Project

Direct Submission

Submitted (01-SEP-2004)

Gene Collection (MGC)

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@mail.nih.gov

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

DNA Sequencing by: The I.M.A.G.E. Consortium (ILLNL)

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 184 Row: j Column: 24

This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.

Location/Qualifiers

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FEATURES

source

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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 3267

Score: 4712.00 Matches: 893

Percent Similarity: 96.54% Conservative: 27

Best Local Similarity: 93.70% Mismatches: 29

Query Match: 93.60% Indels: 4

DB: 9 Gaps: 4

US-09-671-687A-3 (1-949) x BC082001 (1-3267)

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Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80

Db 376 CCTTCTGCTAAGCAAGAAAATCAGATTGGATTAAATCTTAGAGCAACCGATGCA 435

Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99

Db 436 GTTCTGTTTGTGATGAAGGATGTTGTAGAAATAAATAAATAAATTCACAGAGTTACTG 495

Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119

Db 496 TTGGCAATTACCAACTGTGAGGAGAGGCTCAGCCTATTATTAGAAACAGAAATCCGACTA 555

Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuLeuArgSerGlyGlu 139

Db 556 AAAGCGCTCCAGGTAGACGTGGGCGAGTCTCTGTGAGGTACAGCTCGCATCTGGGAGGAG 615

Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159

Db 616 AAGTTTCCAGGAGTTGTACGCTTCAGAGGACCTTTATTATAGCGGAGGACGCTGTCTGG 675

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Db 676 ATTTCTTTGGAGTAGAATTACTGGAAGAAGTCTGTGCCAAGGTTTCACTGATGGGCTG 735
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 736 TATCAAGGAAACACAGCTCTTCCAGTGTGATGAGGACTGTGGCGTGTGTTTGGCATTTGGAC 795
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
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Qy 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 856 GATACAGTCCAGGTTGAACCTCCCCCTTTGGAATTAACCTCCAGAGTTTCTTTGAAGGTT 915
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 916 GGAGAAAGTACAGAATCTGGAAACAGTGATATCTGTGATGTTTACCAGGAAAGAGAGT 975
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 976 CTAGGATATTTTGTGTGTGGATGACATGACCTATTGGCAACTGGGACGGAAGGTTT 1035
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Db 1036 GATGGGGTTCAGCTTTCAGTTTTTGCAGTTTTCAGAGTGTTCAGAGTACAGTTCTCTACACATCAAT 1095
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Qy 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
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Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
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Qy 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
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Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
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Db 1936 TTAGAGATAATGATTGGAAGAAGAAAGGCATCCAGGGCCATTACAATTTCTTTGTTACTTA 1995
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
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Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
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Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
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Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
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Qy 717 LysValGlyValProThrIleGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2356 AAAGTCGGAGTACCCACAATCCAGCAGTTATTAGAATGGTCTTTTATCAACAGCAACCTG 2415
Qy 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2416 AAATTTGCAGAGGCCACCATCATGCTTGATTATCCAGATGCCCTCGGTTTGGGAAAGACTTT 2475
Qy 757 LysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
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Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
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Qy 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
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Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2656 GTTACCTTTCATCCCAAGAGACTGAATACACTTTACCATCCAGATATCACTTCCCAAGAC 2715
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2716 TTGCCCGAGCTGGGACTGGGACACCGCTGCATCCCGTGTGAGAGATGAGATTATTGCT 2775
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Qy 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
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Qy	897	ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu	916
Db	2896	CCACAAGTGACACCTGCCAGAGTAGGAGAGTACTTGAAGATGCTCTGGAGGACCTG	2955
Qy	917	HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr	936
Db	2956	CACCTCTTTGGACTCCAGAAGGATTCAAGGCTGTGCGGCAGACTTCTTTGGATGCATAC	3015
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RESULT 14			
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LOCUS		Primer for synthesizing full-length cDNA and use thereof.	
DEFINITION		BD160617	
ACCESSION		BD160617.1	GI:27866375
VERSION		JP 2002191363-A/15460.	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE		1 (bases 1 to 2845)	
AUTHORS		Ota,T., Isogai,T., Nishikawa,T., Hayaishi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.	
TITLE		Primer for synthesizing full-length cDNA and use thereof	
JOURNAL		Patent: JP 2002191363-A 15460 09-JUL-2002;	
COMMENT		HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/15460 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU PI SAITO, PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUUI OTSUKI PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10, PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof PH Key FT CDS Location/Qualifiers (452)..(2644). 1..2845 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	
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Best Local Similarity:	99.32%	Mismatches:	2
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Qy	92	AsnGluLysPheThrGluLeuLeuAlaIleThrAsnCysGluGluArgPheSerLeu	111
Db	62	AATGAAAGTTACAGAGTACTTTTGGCAATTAACCAATTTGTGAGGAGGTTTCAGCCTG	121

Qy	112	PhelYsAsnArgAsnArgLeuSerLysGlyLeuGlnIleAspValGlyCysProValLys	131
Db	122	TTTTAAAAACAGAAACAGACTAAGTAAGGCCTCCAAATAGACGTGGGTCTGCTGTGAAA	181
Qy	132	ValGlnLeuArgSerGlyGluGluLysPheProGlyValValArgPheArgGlyProLeu	151
Db	182	GTACAGCTGAGATCTGGGGAAGAAAATTTCTTGAGTTGTACGCTTTCAGAGACCCCTG	241
Qy	152	LeuAlaGluArgThrValSerGlyIlePhePheGlyValGluLeuLeuGluGlyArg	171
Db	242	TTACACAGAGGACAGTCTCGGAATATTTCTTGAGTTGAATTCCTGGAAGAGGTCT	301
Qy	172	GlyGlnGlyPheThrAspGlyValTyrGlnGlyLysGlnLeuPheGlnCysAspGluAsp	191
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Qy	211	GluSerAspTyrAlaGlyProGlyAspThrMetGlnValGluLeuProProLeuGluIle	230
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Qy	231	AsnSerArgValSerLeuLysGlyGluThrIleGluSerGlyThrValIlePheCys	250
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Db	602	ATTGGCAACTGGGATGGAAGATTTGATGAAGTCAGCTTTGTAGTTTTGCGTGTGTGAA	661
Qy	290	SerThrIleLeuLeuHisIleAsnAspIleIleProGluSerValThrGlnGluArgArg	309
Db	662	AGTACAAATCTATTGACATCAATGATATCATCCAGAGAGTGTGACGCGAGAAAGGAGG	721
Qy	310	ProProLysLeuAlaPheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsn	329
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Db	782	AAACCAAGGCTCAGAGATCTTACCTCAGACCCTCGAAATAGAAAACAGATCTGAAATATT	841
Qy	349	TyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrp	368
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Qy	369	TyrIleAspGluValAlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPhe	388
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Qy	389	AspArgSerSerProProLeuGlnProProValAsnSerLeuThrThrGluAsnArg	408
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Db	1022	TTCCACTCTTTTACCATTCAGTCTCACCAGAGTGCCTCAATACCAATGGAAATTTGGCCAC	1081
Qy	429	SerProLeuSerLeuSerAlaGlnSerValMetGluLeuLeuAsnThrAlaProValGln	448
Db	1082	AGTCCACTTTCTCTGTGAGCCAGTCTGTAATGGAAGAGCTAAACACTGCACCCGTCCAA	1141
Qy	449	GluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeu	468
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RESULT 15
AX883937
LOCUS
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ACCESSION AX883937
VERSION AX883937.1 GI:40039838
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 18842 07-FEB-2001;
RESEARCH Association for Biotechnology (JP)
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ORIGIN
Alignment Scores:
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QY	192	CysGly---PheValAlaLeuAspLysLeuGluLeuIleGluAspAspThrAlaLeu	210
DB	362	TGTGGCGTGTGTTGTCATTGGACAAGCTAGAACTCATAGAAGATGATGACACTGCATTG	421
QY	211	GluSerAspTyrAlaGlyProGlyAspThrMetGlnValGluLeuProLeuGluIle	230
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DB	1322	GGAACTTTCAGAGCACTCGGTATTTTCACTGTGCCCTGGAAGAGCGCTGTTTGTGAAA	1381
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DB	1382	CTGAAGAGCTGCAGCCCTGACTCTAGGTTTGCATCATTTGCAGCCGGTTTCCAATCAGATT	1441
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
 Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
 Sekine, M., Oabayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
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 Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
 Sugawara, M., Takahashi, M., Kanda, K., Kamehara, K., Furuya, T.,
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 Takeuchi, K., Arita, M., Inose, N., Musashino, K., Yuuki, H., Oshima, A.,
 Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
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 Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,

Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
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 Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
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 Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
 Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
 Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
 Complete sequencing and characterization of 21,243 full-length
 human cDNAs
 Nat. Genet. 36 (1), 40-45 (2004)
 14702039
 JOURNAL
 PUBMED
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 AUTHORS
 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
 Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
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 Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
 NEDO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 2845)
 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing and clone selection:
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.
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 Percent Similarity: 99.32% Conservative: 0
 Best Local Similarity: 99.32% Mismatches: 2
 Query Match: 91.40% Indels: 4
 DB: 8 Gaps: 4
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QY 929 ArgArgLeuLeuCysAspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyr 948
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QY 949 Lys 949
Db 2642 AAA 2644

RESULT 17
AC123449
LOCUS
DEFINITION Rattus norvegicus clone CH230-21D6, *** SEQUENCING IN PROGRESS ***,
3 uncloned pieces.
AC123449
ACCESSION
VERSION AC123449.3 GI:23265406
KEYWORDS HTG; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavares, I., Ceasar, H., Center, A.,
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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
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Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
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Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,
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Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, B., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
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Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
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Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
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Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 241990)
Worley, K. C.
Direct Submission
Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 241990)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 21, 2002 this sequence version replaced gi:21902787.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXOF
Center clone name: CH230-21D6
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 229402 bases at least Q40
Consensus quality: 231763 bases at least Q30
Consensus quality: 231057 bases at least Q20
Estimated insert size: 260790; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* As soon as it is available and the accession number will
* be preserved.
* 1 238985: contig of 238985 bp in length
* 238986 239085: gap of unknown length
* 239086 240731: contig of 1646 bp in length
* 240732 240831: gap of unknown length
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Location/Qualifiers
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clone end:Sp5
site:ECORI

misc_feature end sequence: BH269858"
complement (236297..237124)
/note="clone_boundary
clone_end:T7
site:EcoRI
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/estimated_length=unknown
gap 240732..240831
/estimated_length=unknown

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 241990
Score: 4600.50 Matches: 883
Percent Similarity: 95.29% Conservative: 27
Best Local Similarity: 92.46% Mismatches: 38
Query Match: 91.39% Indels: 8
DB: 14 Gaps: 5

US-09-671-687A-3 (1-949) x AC123449 (1-241990)

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QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
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QY 41 ValProLysGlySerIleGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
DB 205491 GTACCCAAAGGGAGCATAGACAGTACATCCAAGACTGTTTCCGTGGGGCATTTCAAGAGTT 205550
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
DB 205551 CCTTCTGCTAAAGGCAAGAAATATAGATTGGATTAATAATCTTAGAGCAACCGCATGCA 205610
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
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QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
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QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
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QY 160 IlePhePheGlyValGluLeuLeuGluGluGlyValArgGlyGlnGlyPheThrAspGlyVal 179
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QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
DB 206151 CTAGGATATTGTTGGTGTGCACATGATAAACCCTATTGGCAAATGGGATGGAAGGTTT 206210
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
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QY 298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
DB 206271 GACATCATCCAGATAGCGTGACACAGAAAGGAGACCTCCCAAACTTGCCTTATGTCA 206330
QY 318 ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr 337
DB 206331 AGAGGTGTAGTGACAAAGGCTCATCTAGTCATAATAAACCAAGGTTTACAGGATCTACC 206390
QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
DB 206391 TCAGACCTCGAGATAGAAACAGATCTGAATTAATTTATACCTTAAATGGGTTCATCTGT 206450
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
DB 206451 GACTCAACAACAATCCAGTCCAAAACCCATGGTACATTGTGAAGTTTCAGAGAC 206510
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
DB 206511 CCTGCAAGTCACATTACAGAGATGCTTTCAGACTTCGGACATTCATCGCCTCCACCGCA 206570
QY 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
DB 206571 CCTCCTTCCATGAATCCTTGTCTAGCGAGAAACAGATTCCACTCTCTTACCCTTCAGCCTG 206630
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerPro---LeuSerLeuSerAlaG 436
DB 206631 ACAAAGATGCCAACACTAATATGGCAGCATGGCTCACAGTCCACTCTCTCTGTGAGTGC 206690
QY 436 InSerValMetGluGluLeuLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetP 456
DB 206691 AGTCTGTGATGGGGAGCTGAAACAGCAGCGCTGTCCAGAGAGTCCACCTTGCCAGCT 206750
QY 456 roProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProP 476
DB 206751 CTTCTGGAATGGACACGGGCTAGAGGTGGGCTCACTGGCTGAAGTAAAGAGAACCCCC 206810
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QY 556 heGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluG 576
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RESULT 18
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LOCUS Rattus norvegicus clone CH230-3014, *** SEQUENCING IN PROGRESS ***,
DEFINITION 3 unordered pieces.

ACCESSION

AC098162.7 GI:30522215

HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Mammalogathi; Murioidea; Muridae; Murinae; Rattus.

1 (bases 1 to 251132)

REFERENCE

AUTHORS

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biewlat, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrill, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, W., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Louissegh, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartine, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakoeleneh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 251132)

REFERENCE

AUTHORS

Worley, K. C.
Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 251132)

REFERENCE

AUTHORS

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819609.

COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.tgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hasc.bcm.tmc.edu/>

new site: <http://www.hqsc.com>
Contact: hqsc-hel@hcm.tmc.edu

```
----- project information -----
```

Center project name: GGWI.

Center project name: GGWL
Center clone name: CH230-301A

Center clone name: CH230-3014

----- Summary Statistics -----

Assembly program: Atlas 3.0;

Consensus quality: 241087 bases at least Q40

Consensus quality: 243305 bases at least Q30

Consensus quality: 244914 bases at least Q20

Estimated insert size: 256850; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

```

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

*	1	248387:	contig of 248387 bp in length
*		248388	248487: gap of unknown length
*		248488	249536: contig of 1049 bp in length
*		249537	249636: gap of unknown length
*		249637	251132: contig of 1496 bp in length.

FEATURES

source

```

1. .251132
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-3014"

```

misc feature

```

1. 1040
/note="wgs_end_extension
clone_end:Sp6"
1897. 3599
ature

```

misc feature

```

/note="wgs_end_extension
clone_end:Sp6"
complement(6517..7123)

```

misc_feature

```

/note="clone_boundary
clone end:Sp6
site:EcoRI
end sequence:BH292593"
248388..248487
/estimated length=unknown
249537..249636
/estimated length=unknown

```

gap

253

ORIGIN

Alignment Scores:

Pred. No.:

REQ. NO.:
Score: 4600-50

Score: _____
Percent Similarity: _____

Percent Similarity:
Best Local Similarity:

Best Local Similarity:
Query Match:

Length: 251132

Length: 251
Matches: 883

Matches: 88-
Conservative: 27

Conservative: 27
Mis matches: 38

Mismatches: 38
Indels: 9

```
Db 162193 TCAGACCTGGAGTAGAAGACAGATCGAATATATTTATACCTTAAATGGGTCACTGT 162134
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTptTyrIleAspGluValAlaGluAsp 376
Db 162133 GACTCACACACACATCCAGTCCAAACCCATGGTACATTTGATGAAGTTGCAGAGAC 162074
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 162073 CCTGCAAGTCACATTACAGAGATGCTTCAGACTTCGGACATTCATCGCCTCCACCGCA 162014
QY 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 162013 CCTCCTTCCATGAACCTCTGTAGGAGAACAGATTCCACTCCTTACCCCTTCAGCCTG 161954
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerPro--LeuSerLeuSerAlaG 436
Db 161953 ACAAGATGCCAACACATATAGGAGCATGGCTCACAGTCCACTCTCTCTGTGAGTGC 161894
QY 436 InSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetP 456
Db 161893 AGCTGTGATGGGGAGCTGAACAGCACGCTGTCCAGGAGTCCACCCTTGCCAGCT 161834
QY 456 roProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProp 476
Db 161833 CTTCTGGGAATGGACACGGGCTAGAGGTGGGCTCACTGGCTGAAAGTAAAGAGAAACCCC 161774
QY 476 roPheTyrGlyValIleArgTptIleGlyGlnProProGlyLeuAsnGluValLeuAlaG 496
Db 161773 CGTCTATGGGGTTATCGTTGGATTGGCCAGCCAGCCAGGGCTCAGTGACGTGCTGCTG 161714
QY 496 lYLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgT 516
Db 161713 GATTGGAAACCGAAGATGAATGCCAGGTTCCACGGATGGAACTTTTTCAGGGGCGACGGCT 161654
QY 516 YrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAsps 536
Db 161653 ATTTCACTGTGCCCTCGAAGAAACACACTGTTTCGTGAAACTGAAGAGCTGCAGACCACT 161594
QY 536 erArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaP 556
Db 161593 CTAGGTTTGATCCTTCGAGCCTGTTTCCATCAGATCGAAGGTTAACTCTTTTAGCAT 161534
QY 556 heGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluG 576
Db 161533 TTGGGGCTCTACTTAAGTGAAGTAGTAGAAGAAATACGCCACCTAAATGGAAGGAAG 161474
QY 576 lYLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrL 596
Db 161473 GTTTAGAGATAATGATTGGAAAGAAAGAGGATCCAGGGCCATTACAAATCTTGTACT 161414
QY 596 euAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuA 616
Db 161413 TAGACTCAACTTTATCTGCTTATTTGCTTTAGTTCTGCTTCCCTCGACACTGTATTACTTA 161354
QY 616 rgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrG 636
Db 161353 GACCAAGAGAAAGATGACGTAGAGATTATACGTAGACTCAAGAGCTACTGAGGACAG 161294
QY 636 luIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuA 656
Db 161293 AGATAGTCATCTCTGAGAAATATATGGATATGTGTGCCACCAAGATTTATGAAGCTGA 161234
QY 656 rgLysIleLeuGluLysValGluAlaLaserGlyPheThrSerGluLysAspProG 676
Db 161233 GGAAATACTTGAAGAAAGTTGAGGCTGCATCAGGATTTACCTCTGAGGAAAAAGATCCTG 161174
QY 676 luGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleA 696
Db 161173 AAGAAATTTCTAAACATCCTGTTTCATGATATATTTAAGGATGAACCAATGTTTAAATAAT 161114
QY 696 rgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnG 716
```

```
Db 161113 GGTCAAGAGGTCAAAAAGTTCAAGACTGTAACTCTCTATCAAAATTTTTTATGAAAAAATG 161054
QY 716 luLysValGlyValProThrIleGlnGlnLeuLeuGluTyrSerPheIleAsnSerAsnL 736
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QY 736 euLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspP 756
Db 160993 TGAATTTGCGAGGACCAACATCATGCTTGAATATCCAGATGCTTGGTTTGGGAAGACT 160934
QY 756 heLysLeuPheLysLysIlePheProSerLeuLeuLeuAsnIleThrAspLeuLeuGluA 776
Db 160933 TTAAACTATTTTAAAAAATTTTTTCTTCCCTGGGAATTTAAATATGACAGATTTTACTTGAAG 160874
QY 776 spThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysT 796
Db 160873 ACATCCAGGACGTGCCCATCTGTGGAGACTCGCCATGTATGATGATGATGATGATGATG 160814
QY 796 yrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrG 816
Db 160813 ATGATGACCCGGACATCTCGGACGGGAAGATCAAGCAGTTCTGTAAAGACCTCGCAGCACTC 160754
QY 816 InValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysA 836
Db 160753 AGGTTCACTTTTCATCCCAAGAGACTGAATCACTTACCATCCAGTATCACTTCCCAAAG 160694
QY 836 spLeuProAspTyrAspTyrArgHisGlyCysIleProCysGlnAsnMetGluLeuPheA 856
Db 160693 ACTTGGCCGACTGGGACTGGAGACATGGCTGCATCCCATGTGAGAGATGGAGTTATTG 160634
QY 856 laValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspS 876
Db 160633 CTGTGCTCTGCATAGAAACCAAGCCACTATGTTGCTTTTGTGAAGTACGGGAAGGATGACT 160574
QY 876 erAlaTyrLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnI 896
Db 160573 CTGCTGGCTCTTCTTTGACAGCATGGCTGATCGAGATGGTGTGAGATGCTCAGAAATGGCTTCAACA 160514
QY 896 leProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspL 916
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QY 916 euHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaT 936
Db 160453 TGCATCTTTGCACTCCAGAAAGGATTCAAGGCTGTGCGGCAGACTTCTTTTCGGATGCAT 160394
QY 936 yrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
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Search completed: January 16, 2006, 11:32:32
Job time : 4353 secs